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September 23, 2004, 23:33:46; Search time 73.5819 Seconds (without alignments) 1509.371 Million cell updates/sec
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1760
1 MVKALVIINCIILAIGNCGG......QQEESQETEQSSLSRPISEC 352
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
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1: sp archea:*
2: sp_bacteria:*
3: sp fungi:*
4: sp_human:*
5: sp_invertebrate:*
5: sp_mammal:*
5: sp_mhc:*
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Gapop 10.0 , Gapext 0.5
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sp.rodent:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9fz95 arabidopsis	P93010 arabidopsis	Q94gbl arabidopsis	Q9fz96 arabidopsis	Q9m7rl arabidopsis	Q8h7p2 oryza sativ			049724 arabidopsis	Q91pf6 arabidopsis	049725 arabidopsis	-	Q9zuh3 arabidopsis	09sy29 arabidopsis	049722 arabidopsis	Q8s170 oryza sativ
SUMMARIES	OI.	Q9FZ95	P93010	Q94GB1	Q9FZ96	Q9M7R1	Q8H7P2	049726	QBRY74	049724	Q9LPF6	049725	Q7X7P4	Q92UH3	Q9SY29	049722	Q8S170
	DB	101	10	10	10	10	10	10	10	10	10	10	10	10	70	10	70
	Query Match Length DB	351	356	358	356	356	399	344	377	1128	379	348	751	315	382	358	372
de	Query	99.1	65.3	65.3	64.1	63.9	39.3	31.7	31.6	31.6	31.6	31.6	30.3	30.1			
	Score	1744.5	1149	1149	1128	1124	691.5	557.5	557	557	556.5	555.5	534	530	516.5	502.5	492
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17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

		1;	· 09	120
T 1 OPPEZOS PRELIMINARY; PRT; 351 AA. OPPEZOS O1-WAR-2001 (TrEMBLrel. 16, Created) O1-JUN-2003 (TrEMBLrel. 16, Last sequence update) O1-JUN-2003 (TrEMBLrel. 24, Last annotation update) O1-JUN-2003 (TrEMBLrel. 24, Last annotation update) O1-JUN-2003 (TrEMBLrel. 24, Last annotation update) F3H9.12 F3H9.12 F3H9.12 F3H9.12 F3H9.13 F3H9.12 F3H9.12 F3H9.13 F3H9.13 F3H9.14 F3H9.15 F	0. MW; 992F1704CB76ED70 CRC64;	Score 1744.5; DB 10; Length 351; Pred. No. 5.1e-118; 0; Mismatches 0; Indels 1; Gaps	MVKALVIINCIILAIGNCGGBLIMRLYPNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR 60	61 RRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI 120
T 1 5 GPF295 GPF295 GPF295; O1-WAR-2001 (TrEMBLrel. 16, Created) O1-WAR-2001 (TrEMBLrel. 16, Last sequen O1-UNO-2003 (TrEMBLrel. 24, Last annota F3H9.12. F3H9.13. F3H9.13. F3H9.14. F3H9.15. F3H9.15. F3H9.15. F3H9.15. F3H9.16. F3H9. F3H9.16. F3H9.16	InterPro; IPR004853; DUF250. Pfam; PF03151; DUF250; 1. SEQUENCE 351 AA; 38871 MW;	Query Match 99.1%; Best Local Similarity 99.7%; Matches 351; Conservative	1 MVKALVIINCIILAIGN 	RRSNNVGDSTSFFLIKP
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352

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121 AIFSFEWUKHKFTPFTINAVVLLTVGAAVLGMHTBTDKPVHBTHKQYITGFLITVAAAVM 180
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EMBL, AF078532, AAK61813.1; -1.

InterPro: IPR040853; DUF250.

Pfant, PF03151; DUF250; 1.

NON TER 358 358 358 .... CATABARA CRC64;
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                                                                                                                                                                LAVIFYHEKFQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPIS
241 RVIAGEARDFKLGESLYYVVIVFTAIIMQAFFVGAIGLIFCASSLVSGIMVSALLBVTVI
                                                                                                                                                                                      QALPKEAREFKLGEALFYVVAVFSALIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabiopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 AA; 39461 MW; 69709A0EA6ECD6A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. C 24;
MEDLINE=20129770; PubMed=10662864;
Gillissen E., Burkle L., Andre B., Kuhn C., Rentsch
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OEC-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 60.4
Matches 218; Conservative
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RRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI 120
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                                         AIESEFWYKHKFTPFTINAVYLJTVGAAVLGMHTBTDKPVHETHKQYITGFLITVAAAVM
                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                          QAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISEC 352
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SEQUENCE 356 AA; 39201 MW; CD5BCAEA31BE63E6 CRC64;
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Last annotation update)
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Matches 218; Conservative
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STRAIN=cv. Columbia;
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                                                                                                                                                                                                                                                                                           294 IFYHEKFQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISE 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A new family of high-affinity transporters for adenine, cytosine, and
                                                                               VAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
MEDLINE=20129770; PubMed=10662864;
Gillissen B., Burkle L., Andre B., Kuhn C., Rentsch D., Brandl
Frommer W.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 356;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
Purine permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.9%; Score 1124; DB 10; Best Local Similarity 59.8%; Pred. No. 2.7e-73; Matches 214; Conservative 66; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purine derivatives in Arabidopsis.";
Plant Cell 12:291-300(2000).
EMBL; AF078531; AAF6547.1; -.
GO: GO:0016020; C:membrane; IEA.
InterPro; IPR004853; DUF250.
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303 LAVICFQEKFQAGKGVALALSLWGSVSYFYGQVKSEE-----KTKAQDTQLSQL--PVT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.P., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao Q., Chin C., Chiou J., Choi E., Gonzalez A., Howng B., Johnson-Hopson C., Khan S., Kim C., Kor T., Lee J.M., Tenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                Purine permease.
F3H9-12 OR ATIG28230/F3H9-10 OR ATIG28230.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,

Yamada K., Chan M.M., Tang C., Toriumi M., Wong C., Wu H.C.,

Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,

Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Columbia,
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Seki M., Iida K., Kamiya A., Narusaka M., Carninci P., Kawai
Hayashizaki Y., Shinozaki K.,
"Arabidopsis Y., Shinozaki K.,
"Arabidopsis to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis A.;
"Arabidopais Open Reading Frame (ORF) Clones.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO31.043 AAF99432.1;
EMBL; AK117664; BAC42317.1;
EMBL; BT005504; AAO63924.1;
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                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; D86408; D86408.
GO; GO:0016020; C:membrane; IEA.
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InterPro; IPR000620; DUF6.
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Matches 215; Conservative
                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                D 355
                                                 E 351
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                                                                                                                                                                                                                                                          Q9FZ96;
01-MAR-2001
                                                 351
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VCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSG--KKVVDKPQPPETELPIL--PVSD 353

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65 NVGDSTSFFLIKPRLLI-AAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|: |: || |: || :: || :: || GIGN-----LLIPRRLVGAAAVLGGLYAVSCFVYALGSQALPLSTSSLLLATQLAFTAVF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPEMVKHKETPFTINAVVILITVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ILPLVELAYQK-----AKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIF 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSN
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
T9A21.70 (R AT421822)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyte; Viridiplantae; Streptophyte; Embryophyte; Tracheophyte;
Spermatophyte; Magnoliophyte; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NTBL TaxID=3702;
                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Score 691.5; DB 10; Length 399; 43.1%; Pred. No. 4.4e-42; Live 71; Mismatches 107; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 YHEKFQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wing R.A., YU Y., Soderlund C., Kim H.-R., Rambo T., Saeki Currie J., Collura K.;
"Rice Genomic Sequence.";
Submitted Genomic Sequence.";
EMBL, ACI21 (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ACI21 (NOV-2003) ANN64138.1;
InterPro; IPR004853; DUF250.
PFam, PF03151; DUF250; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1 protein.
399 AA; 41487 MW; D180480A4081416A CRC64;
                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149; Conservative
                                                              PRELIMINARY;
                                                                                                                                                                                                          Hypothetical protein.
OJ1217B09.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 35
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                                                                 Q8H7P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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VFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLALS 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 FTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPLVELA 191
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                                                                                                                                                                                                                                                                                                                                                                   12 ILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNNVGDSTS
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                       DB 10; Length 344;
                                                                                       K., Mayer
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      Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley Bancroft I., Mewes H.W., Mayer K., Schueller C.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      Match
Local Similarity 35.3%; Pred. No. 1.7e-32;
Les 120; Conservative 72; Mismatches 131; Indels
                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021713; CAA16794.1; -.
EMBL; AL161548; CAB78824.1; -.
                                                                                    Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 344 AA; 37819 MW; 28795F066738D8B1 CRC64;
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Last sequence update)
Last annotation update)
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01-UN-2002 (TERMBLEEL 21, La
01-CCT-2002 (TERMBLEEL 22, Lak
Hypothetical protein.
                                                                                                                                                                                                                   PIR; T04924; T04924.
Interpro; IPR004853; DUF250.
Pfam; PF03151; DUF250; 1.
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SEQUENCE FROM N.A.
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FROM N.A.
                                                                             SEQUENCE FROM
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS--NNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 IAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAV 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 MYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEARE 239
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                                                                                                  SEQUENCE FROM N.A.

A Yamada K., Banh J., Chang C.H., Chang E., Dale J.M.,
A Yamada K., Banh J., Lee J.M., Onodera C.S., Quach H.L.,
Deng J.M., Ordulamith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Sakurai T., Satou M., Arusaka M., Nguyen M., Palm C.J.,
Davis R.W., Ecker J.R., Theologis A.,
Tarae (ORF) Clones.",
L Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL, AY095558; AAM20208.1;
R EMBL, AY095558; AAM20208.1;
R EMBL, AY095559; DUF250.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
19A21.50 OR AT4G18200.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; wannoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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     to the EMBL/GenBank/DDBJ databases.
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Bancroft I., Mewes H.W., Mayer K., Schueller C.,
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 377 AA; 41786 MW; B77A09A4289859AB CRC64;
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Matches 125; Conservative
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Submitted (JAN-2002)
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049724
AC 04973
DT 01-4
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                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                              2 VKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRR
                                                                                                                                                                                                                                                                                                                                                                                           62 RS--NNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 MYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 FKLGEALPYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. Columbia;
Liu S., Vaysberg M., Sakano H., Lee J., Lenz C., Pham P., Toriumi M.,
Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B.,
Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.,
Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
Nguyen M., Palm C., Shinn P., Southwick A., Davis R., Ecker J.,
Federspiel N., Theologis A.;
The sequence of BAC T12C2; from Arabidopsis thaliana chromosome 1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                      31.6%; Score 557; DB 10; Length 1128; 36.1%; Pred. No. 6e-32; Live 76; Mismatches 131; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1084 MDASKIFSIILAIWGFLSFVYQHYLD-EKKLKTCOTKPVEEFTOTL 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 FQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSL 345
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021713; CAA16792.1; -.
EMBL; AL161548; CAB78822.1; -.
PIR; T04922; T04922.
InterPro; IRR004853; DUF250.
Pfam; PF03151; DUF250, 3.
Hypochetical protein.
SEQUENCE 1128 AA; 124621 MW; 9B1B88BFA0DE9E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09LPF6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
112C22. 2 protein (Hypothetical protein).
112C22. 2 OR ATIG44750, T12C22. 2 OR ATIG44750.
Arabidopsis thaliana (Mouse-ear cress).
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Best Local Similarity 36.18
Matches 125; Conservative
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FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 LVSVNIFFLIGGQAASVLIGREYYDEGGNSKMMATLVQTAAFPILYIPLLL----LPSSA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                  Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T., Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A., Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T., Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 LPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1940thetical protein.
1940thetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyta; Magnollophyta; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacee; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                           31.6%; Score 556.5; DB 10; Length 379; 34.4%; Pred. No. 2.3e-32; Live 89; Mismatches 121; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley Bancroft I., Newes H.W., Mayer K., Schueller C.; submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                 Davis R.W.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
      Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                           1 protein.
379 AA; 41289 MW; FIED85A70FAD7001 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                   EMBL; AC020576; AAF78258.1; -. EMBL; AY062782; AAL32860.1; -. EMBL; BT003358; AAO29976.1; -.
                                                                                                                                                                                                                                                                                                                  PIR, D96506, D96506.
InterPro, IPR004883; DUF250.
Pfam, PP03151, DUP250; 1.
Hypothetical protein.
SEQUENCE 379 AA, 41289 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 115; Conservative
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Best Local Similarity
                                                           SEQUENCE FROM N.A.
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NCBI_TaxID=3702;
                                                                                                                                                                                                                                        Submitted
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049725
1D 04972
AC 04972
DT 01-07
DT 01-07
DE HYPO
GN T79A2
OC SPER
OC SPER
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OC SPER
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BARD B., FENG Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y., Lu Y., Li G., Li T.,
Zhang Y., Hu H., Jia B.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.; sheng H.H.,
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 VGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPLVELAYQKAKQTMSYTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 LEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLG
                                                                                                                                                                                                                                                                                                                                                           26 LYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNNVGDSTSFFLIKFR-LLIAAV
                                                                                                                                                                                                                                                                                                                                                                                            25 VYYDNGGNSKWLATVVQLVGFPVLLFYYILSFKTHATTDRDGKRTS-----PRNRVLVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 IVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFWVKHKFTPFTINAVVLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                             DB 10; Length 348;
                                                                                                                                                                                                                                                             31.6%; Score 555.5; DB 10; Length 36.7%; Pred. No. 2.5e-32; Attive 72; Mismatches 120; Indels
il protein.
348 AA; 38556 MW; 354CB8D6D5547786 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0SJNBA0013X16.25 protein (OSJNBb0016D16.5 protein).
OSJNBA0013X16.25 OR OSJNBB0016D16.5.
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318 LDDKNLKKNHEITTTESPDPPEAEEST
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Query Match
Best Local Similarity 36.7%
Matches 120; Conservative
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RESULT 14
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                                                                                                                                                                                                      63
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MEDLINE-20083487; PubMed=10617197;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F., Submitted (SBP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, ALG62557, CAR03776.1;

EMBL, ALG66589, CAE04314.1;
                                                                                                                                                                                                                    EALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAE
                                                                                                                                                                                                                                                                                                                                                                                       ILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLG
                                                                                                                                                                                                 4 ALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRS
                                                                                                                                                                       Gaps
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                                                                                                                                                                    92; Mismatches 133; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::: :::|||:|| | 340 KIVAMLIAIWGFISYLFQHYLDGKKAKASSGDSVRGQEDVVAESDKST 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 KGLSLALSLWGFVSYFYGEIKSGE-----DKRRIQQEESQETEQSS 344
                                                                                                                                       DB 10; Length 751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005967; AAD03383.1; -.
PIR; A84634; A84634.
                                                                                                        751 AA; 79987 MW; 714C08319D7B5FD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                     30.3%; Score 534; DB 10; 30.9%; Pred. No. 1.8e-30;
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                                                                                                                                                    Local Similarity 30.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:761-768(1999)
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 INAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPLVELAYQKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 IWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLALSLWGFV
                                                                                                                                                                                                                                                                 LIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNNVGDSTSFFLIKP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 QTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAI
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta;
dons; core eudicots; rosids;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dewar K., Feng J., Kim C., Li Y., Sun H.,
Kurtz D., Oji O., Shen Y.K., Toriumi M.,
Davis R.W., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                 30;
                                                                                                                                Length 315;
                                                                                                                                                                                                 Indels
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                                                                C7658FFABD4B3814 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TJTH7.15 (Hypothetical protein).
                                                                                                                         Match 30.1%; Score 530; DB 10;
Local Similarity 35.5%; Pred. No. 1.5e-30;
GB 117; Conservative 71; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ
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                            Pfam; PF03151; DUF250; 1.
SEQUENCE 315 AA; 33847 MW;
IPR004853; DUF250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Buehler E., Shinn P.,
Conway A., Conway A.,
Vysotskaia V., Yu G.,
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Submitted (FEB-1998)
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Submitted (MAY-1998)
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InterPro;
                                                                                                                             Query Match
Best Local S:
Matches 117
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307 SLALSLWGPVSYFY----GEIKSGEDKRRIQOEESQETEQ 342 :: |::||||||| | : | :| :| :| :| :| :|
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InterPro; IPR004853; DUF250.
                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06,
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                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                    049722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 ALIIASQLAFIAIFSFFWVKHKFTPFTINAVVLLTVGAAVLGMHTETDKFVHETHKQYIT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 GFLITVAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDF 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Yamada K.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVK-----ALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPL
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,

Yamada K., Chan M.M., Tang C., Toriuni M., Wong C., Wu H.C.,

Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,

Shida J., Jones T., Kamiya A., Satou M., Seki M., Shinn P.,

Southwick A., Tripp M.G., Wu T., Satou M., Seki M., Shinn P.,

Theologis A.,

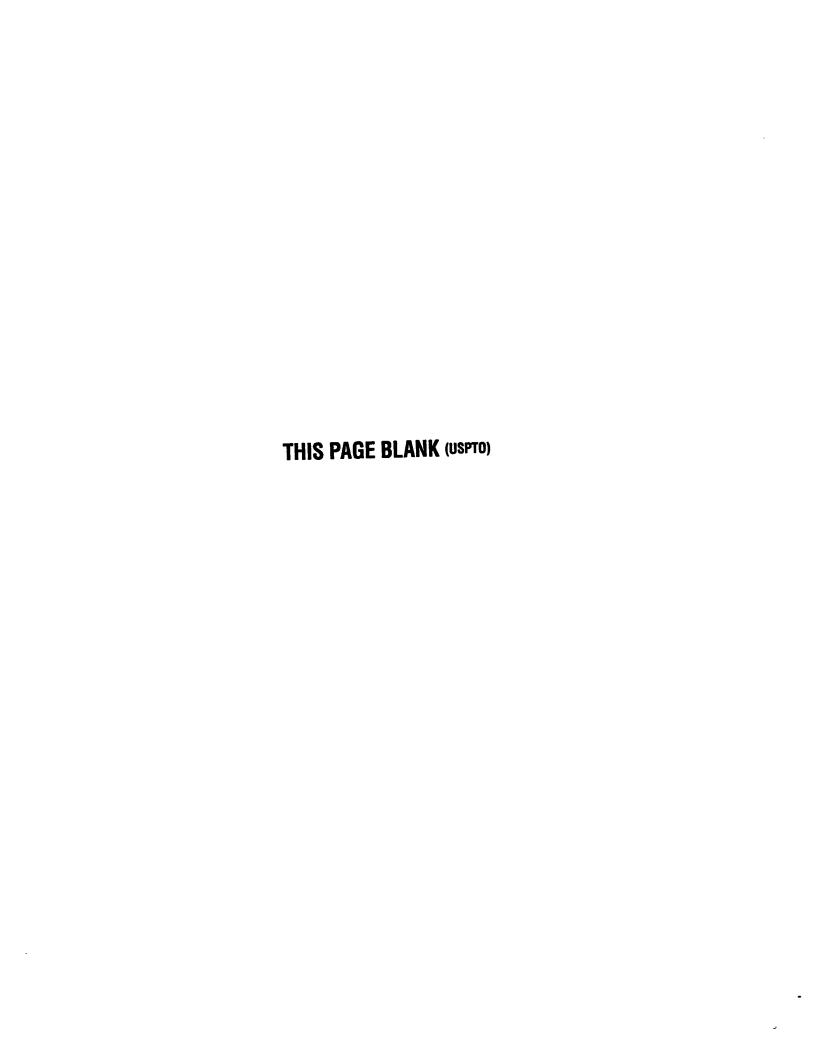
"Arabidopsis Full Length cDNA Clones.",

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%; Score 516.5; DB 10; Length 382; 32.2%; Pred. No. 1.7e-29; ive 81; Mismatches 132; Indels 29;
                                                                                                                                                                                       Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX064151; AAD32940.1; -.
EMBL; AX06461; AAM61204.1; -.
EMBL; BT004160; AAM61204.1; -.
EMBL; BT005495; AAM6318.1; -.
GO, GO:0016020; C:membrane; IEA.
InterPro; IPR004853; DUF250.
InterPro; IPR004850; DUF6.
Pfam; PF00892; DUF6; 1.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
                                                                                                                                                                                                                                                                                                                                    "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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382 AA; 42320 MW; E030A23A8C834ACA CRC64;
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Genome Biol. 0:0-0(2002).
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Feldmann K.;
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Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
19A21.30 OR AT4G18190.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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28.6%; Score 502.5; DB 10; Length
Best Local Similarity 33.2%; Pred. No. 1.7e-28;
Matches 113; Conservative 80; Mismatches 120; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021713; CAA16790.1; -.
EMBL; AL161548; CAB78821.1; -.
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358 AA; 39552 MW; FDD45970C1CF1600 CRC64;
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311 AMFLAIWGFVSYGYQHYVNDRKPEEDQELPQSKEEEEQKQ 350

Search completed: September 23, 2004, 23:49:47 Job time : 75.5819 secs



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Gillissen, B., Andre, B., Rentsch, D., Buerkle, L., Kuehn, C., Brandl, B.
and Prommer, W.B.
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Gillissen, B., Burkle, L., Andre, B., Kuhn, C., Rentsch, D., Brandl, B. and Frommer, W.B.
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Submitted (15-JUL-1998) Institut fuer Botanik, University of
Tuebingen, Auf der Morgenstelle 1, Tuebingen, Baden-Wuerttemberg
GGGATTGTGTTTTGTGCATCACTAGCTTCTGGTGTTCTGATAAGTGTTCTGCTTCCG
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RESULT 4 BT005504 LOCUS DEFINITION

ORGANISM

REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TACTITATATICTTACGGATTAGCATATCTGCCAGTTTCAACTTCATCGCTCATAATCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 CCTTTGTTAACTCGTCTTCTACTTCACCAATGGCGGAAAACGAATCTGGTTCATGAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 CGCCGCGGCAACCGCAACCCTAACAACGCGGAAACAAGCGGAAAACAAAGCTCTTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                              /evidence=experimental
produce=rputative purine permease"
/protein_id="AAO63924_1"
/db_xref="GI:28973199"
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                                                          1. .1102
/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                 /ecotype="Columbia"
/note="This clone is in pUNI 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 845; DB.
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WDKPQPPETELPILPVSDYVA"
                                                                                                            /mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
/clone="U50269"
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            /gene="At1g28230"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1072. .1102
/gene="At1g28230"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.6%;
Matches 1045; Conservative
          submitted to Genbank
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Arabidopsis thaliana clone U50269 putative purine permease
(AL1928230) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                            1048
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, viridiplantae, streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z [bases 1 to 1102)
Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., WL,H.C., Yu,G., Yuan,S., Carninci,F., Chen,H., Cheuk,R., Hayashizaki,Y., Nguyen,M., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Suthwick,A., Tsipp,M.G., Wu,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: 'RIKEN Arabidopsis Pull-Length CDNA): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
GIGACTGAAGTTTTCGCCGTCGTTTGTTTCCGGGAGAAGTTTCAGGCAGAAAGGTGTC 960
                                                                                                                                                                                                                                    988
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                                                                                                                                                                                                                                                                                                                         989 TCTCTACTTCTCTTTGGGGATTTGTCTCTTACGGGGAGTTTAAATCCGGC
                                                                             GGGATTGTGTTTTTGTGCATCATCACTAGCTTCTGGTGTTCTGATAAGTGTTCTGCTTCCG
                                                                                                                                                                                                                         GTGACTGAAGTTTTCGCCGTCGTTTGTTTCCGGGAGAAGTTTCAGGCAGAAAGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                 C. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed
s work. Shinozaki, K. (RIKEN GSC) and Theologis, A.
contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                      1021 AAGAAAGTIGITGATAAACCTCAACCGCGGAGACAGAACTGCCTAITCTTCC
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6 CTOCOTOMAMATCACTICCOCTTGACTTGACTTGACTTGACTTGACTTGACTTGACT	Mukharsky, N., Pham, P., Sakano, H., Schwartz, J., Shinn, P., Thaveri, A., Toriumi, M., Vaysberg, M., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Theologis, A. and Davis, R.W. Direct Submission Submitted (29-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA (CA) (CA)		Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologiand Davis, R.W. and Davis, R.W. Direct Submisted (11-Aug-2000) DNA Sequencing and Technology Center, Submitted (11-Aug-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 9430 USA (Gases I to 121720) (Ghasell, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,	Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Ineclosis,A and Davis,R.W. E Direct Submission NAL Submitted (15-AUG-2000) DNA Sequencing and Technology Center, Stamford University, 855 California Avenue, Palo Alto, CA 94304,		http://gnomic.beanton.com/ (S.M. Hebegaard, et al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html). Location/Qualifiers source 1.21720 /mol-type="genomic DNA" /mol-type="genomic DNA" /chromosome="1"	/clone="F349" misc_feature 17373 /note="vorlap with bases 96,792-104,163 of IGF BAC clone /note="vorlap with bases 96,792-104,163 of IGF BAC clone F3M18, gb AC010155, see GenBank record for clone F3M18 for annotation in this region." gene /note="F349.1" /no	1	/product="dormancy-associated protein" /protein_id="AAF98422.1" /db_xref="G1:9795604" /translation="MVLLEKLWDDVVAGPQPDRGLGRLRKITTQPINIRDIGEGSSSK
GCTCCTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCCAATGGTCATGTGCTTGAGATTCCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCCAATGGTCTTGGTGTGTGT	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE	TITLE JOURNAL REFERENCE	TITLE	COMMENT	FEATURES	E 01 (•	
GCTCGTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCCAATGGTCATGTGCTTGAGATTCCAATGGTCATGCTTGAGAATTCCAATGGTCATGGTCTTGAGATTCCAATGGTCATGCTTGAGATTCAAGAATTCAAGAATTCCACTTGAGAATTTAAGGTCATGCTTGAGAATTTTAAGGTCATGGTCATGGTCATGGTCATTCAT									
	GCTCGTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCAGATGGTCATGTGCCTTGCT	GGAATAATATGGCAAGGTTTCTTCTTAGGAGCCATAGGGATTGTGTTTTGTGCATCATCATCATCATCATCATCATCATCATCATCATCATC	TGTTTCCGGGGAGAAGTTTCTCTTTGGGGGAAGGTGTCTCTCTTTTGGGGAAGGTGTCTCTCTTTTTGGGGAAGGTGTCTCTCTTTCTCTTTTGGGGAAGGTGTCTCTCTTTCTCTTTTGGGGAAGGTGTCTCTCTTTCTCTTTTGGGGAAGGAA	045 CCGCCGGGACACACACTGCTTCC 1073 	AC021044 121720 bp DNA linear PLN 3 Arabidopsis thaliana chromosome I BAC F3H9 genomic sequen complete sequence. AC021044 AC021044.5 GI:8347959 HTG. Arabidopsis thaliana (thale cress) Arabidopsis thaliana (thale cress) Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Trac Eukaryota, Wirdiplantae, Streptophyta; Embryophyta; Trac Spermatophyta; Magnoliophyta; eudicotytadons; Orre eudico		Unpublished Unpublished (Loases 1 to 121720) 2 (bases 1 to 121720) 2 (bases 1 to 121720) 3 Lafei,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,O., Buthler,E., Chin,C., Chlou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo, T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,	Direct Submission Submitted (12-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, ISA	Joses 1 to 121720) Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen Federspiel, N.A., Palm, C.J., Conway, A.B., Bei, Q., Bueh Altafi, H., Nguyen, M., Lam, B., Southwick, A., Bei, Q., Bueh Chin, C., Chiou, J., Choi, E., Dunn, P., Gonzalez, A., Howng, Koo, T., Lee, J.M., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S.

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PVYPPKFNRSLVAVRGTVYCKSCKYAAFNTLLGAKPIEGATVKLVCKSKKNITAETTT
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                                                                                                                                                                                                                                                         /tränslation="MGFIGKSVLVSLVALWCFTSSVFTEEVNHKTQTPSLAPAPAPYH
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                                                                                                                                                                                                                                                                                                         PTKPPVKPPVSPPAKPPVKPPVYPPTKAPVKPPTKPPVKPPVYPPTKAPVKPPTKPPV
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                                           ATSSSMPPEDHAYVGSSDDQVLDWL"
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Gane="Rays,6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               crcrrdgrcrccrrccrcagccgrcgccaccaccaccacccraaccaccacaaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAACAGCAAGCAAGAAGAAGAAGAATGAAGAATGGTTTGATAATCATAAACTGTATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCACTATAGGAACATGTGGAGGTCCTTTGTTAACTCGTCTTCACTTCACCAATGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCGGGATCCTTGCGTTACACAGTGATGGAGACAAAACCGGCTAAGGAGAGAAGAAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACGAATCTGGTTCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCATCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTTGGTCTCCTTCCTCAGCCGTCGCCGCGCAACCGCAACCCTAACAACGCGGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGTCAAGCAAAAGTTCACTCCCTTCTCCCATAAACGCCGTCGTTTTGTTGACGGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGTGGTTGTTGATGACTGTGGTTGCAGCTCTTCTATGCTTTATATTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAACAGCAAGCAAGAAGAAGAAGAATGGTTTGATAATCATAAACTGTATTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCACTATAGGAACATGTGGAGGTCCTTTGTTAACTCGTCTCTACTTCACCAATGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGAATCTGGTTCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCATCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCGGAAAACAAAGCTCTTCCTCATGGAAACTCCTCTGTGGAGCGCCTCCATTGTCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGTTGCTCACAGGACTTGACAACTACTTATATTCTTACGGATTAGCATATCTGCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTTGCTCACAGGACTTGACAACTTATTATTTCTTACGGATTAGCATATCTGCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAACTTCATCGCTCATAATCGGAACTCAACTAGCTTTCAACGCTCTCTTCGCTTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 530; DB 8; L
Pred. No. 1.1e-286;
0; Mismatches 4;
                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                    43.3%;
ilarity 99.5%;
Conservative 0
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Best Local Similarity
Matches 730; Conserv
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24148. .24395)
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EQRAD I LTKALVRMKFKEMRDLI GVQDEL I LSETEQI NI QQGQASYMQTLKRQAKVDS
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DGDSLS YPFENETT I RNREKDRLALE I FGPESTDDSDESGTEBEFMETNLMSLVSLQM
GKRGKRSMRKGTWARTLLENHVGQHKNTQDBVKNCLYCETLVHSFSI LI GVVSMMQM
I QVILLVSMDASVI PNLQNPQVSCKRNVTLKSLCEVCLI LT
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                                                                                                                                                      /note="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Hypothetical protein"
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GKSSFVFGALMTTYRLCNSNFSYYULLIAKTIAKEGNICABEGSFEKSSYLMOK
CNALIGGSVFGEGEDUSGWSFLKEMLRRKICPDIATFINILINVLCAEGSFEKSSYLMOK
CNALIGGSVFKEGEDUSGWSFLKEMLRRKICPDIATFINILINVLCAEGSFEKSSYLMOK
MEKGSTAPTIVTYRTVLAHVCKKGRFRAALELLDHRKSKGVDADVCTYNMLIHDLCRS
MEKGSTAPTIVTYRVLAGENEWTATLINGFSNEGKULTASQLLLMEMLSFGELSPHIV
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KMRANGVCVGRITYTGMIGDCLCKNGFLDEAVVLLARMSKGGIDPDIVTYSALINGFCK
NGRFRTAKEIVCRIYRVGLSPNGITYSTLINGTCKASALINGFCK
UGRFRTAKEIVCRIYRVGLSPNGITSTLINGTLENTENDHYTYSALILGAFREND
FTRNULTSLCKAGKRARAREPRENTGMISGLENGTARTHAND
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VNKERNIAHTCPPRVARARARARAKCGRADBATLLLRRMLKMKLVPTIASFTTLMH
VNKERNIAHTCPPRVARARARARAKCGRADBATLLLRRMLKMKLVPTIASFTTLMH
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ALQNDIAVCHREELDLOSWULJSCHALFELCLIHTSSRSJSLYCYTEQDRGOSGGAT
LLARFSDRYNNSKTTPKESLIESLKLPGGLINAVFNSTCIKDLVCLEVSXTLLDSLAKSF
FTERTROEWGRENDAN
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
Address for correspondence: kaos@kazusa.or.jp
Address for correspondence: kaos@kazusa.or.jp
Address for information on annotation of this clone, please see
For the latest information on annotation of this clone, please see
Attainilarity to proteins in the databases are described in
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
ERNSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CES, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NatGene2)) and
Splicebredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgl-bin/sp.cgl),
http://genme.wustl.edu/eddy/tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
fins sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MDF20 and the 3' clone is MYN21.
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pgKSSEGHVKSGGODPSKRPOPKKWLCCMQAPAVDS"
join(15029. .15205,15277. .17049)
/note='gene_id'MWJ3.4"
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/db_xref="G1:8843735"
/translation="MCLTKDINILGSYETGFDMEKSIYNILTIDRWGSLNHMDYRQAR
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iklyMGKLAKPLKPLKPLKONSNPSVYDILIRVYLREGMIQDSLEFRLMGGLYGFNBSVYT
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/strain="Columbia"
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/clone="collap"
/clone="co
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note="gene id:MWJ3.3"
codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-JUN-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jun 30, 1998 this sequence version replaced gi:2673800. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from B.coli, yeast, vector,
                                                                                                                                                                                       PPSCO4066 5947 bp DNA linear INV 27-JUN-1998 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-66, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Spermatophyta, Magnoliophyta, Eudicotyledons, core rosids, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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DNA Res. 7 (1), 31-63 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (O6-OcT-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana genomic DNA, linear PLN 27-DEC
AB018120 BA000015
AB018120.1 GI:3702738
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 5947)
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100.0%; Pred. No. 0.88;
tive 0; Mismatches 0; Indels
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Corganisma="Plasmodium falciparum"
/mol_type="qenomic DNA"
/db_xref="taxon:5833"
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Nakamura, Y.
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SELDVMMRSRTCLEKKVPLELVNSDPRVTIGSSHGWVATLKEDGILERLQDDLNPVAS
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                                                                                                                                                                                                                                                                                                                                                                                               QVBAVRASENETLKKLETTQEEIKKLKTATEEALKKAAMADAAKKAVEGELRRWRERD
QKKAEBAATRILAEAEMKMASESSPQQHYKAPKQKPVNNKLEKTKTSVVSKKVLMPNL
SGIFNRKKNQVEWGSPSYLPGEKPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTAAHATTSNIJSSPPEFTPDQIRVITQMIQNRNNGTSDKLSGRWKLGDVILDTGASH
HMTGQLSLLTNIVTIPSCSVGFADDRKTFAISMGTFKLSETVSLSNVLYVPALNCSLI
SVSKLVKQIKCLALFTDTICVLQDRFSRTLIGTGEERDGVYYLTDAATTTVHKVDVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSLIHCDVWGPYRVPSSCGAVYFLTIVDPSRSVWTYLLLAKBEVRSVLTNFLAYTEK
QFGKSVKIIRSDNGTEFMCLSSYFKEQGIVHQTSCVGTPQQNGRVERKHRHILNVSRA
LLFQASLPIKFWGEAVMTAAYLINRTPSSIHNGLSPYELLHGCKPDYDQLRVFGSACY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHRVTRDKDKFGERSRLCIFVGYPFGCKGWKYYDLSTWEFIVGRDVVFRENVFPYATN
EGDTIYTPPVTCFITYDEDWLPFTTLEDRGSDENSLESPPPVCYTDVSESDTEHDTPQS
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QLARLKDYILYNASCTPNTPHVLSPSTSQSSSSIQGNSQYPLTDYIFDECFSAGHKVF
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TKFNADGTVERYKARLVVQGNNQI EGEDYTETPAPVVKMTVRTLLRLVAANQMEVYQ
MDVHNAPLHGDLEBEVYMKLPPGFRHSHPDKVCRLRKSLYGLKQAPRCWFKKLSDALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKLKYFLGIEVSRGPDGIFLSQRKYALDIISDSGTLGARPAYTPLEQNHHLASDDGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFGFIQGYEDYSFFSYSCKGIELRVLVYVDDLIICGNDEYMVOKFKEYLGRCFSMKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHALWHQRLGHPSFSVLSSLPLFSGSSCSVSSRSCDVCFRAKQTREVFPDSSNKSTDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDCHSVRDAVRDGIITTHHVRTSEQLADIFTKALGRNQFIYLMSKLGIQNLHTPT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pir||T05237
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to unknown protein"
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pir||T05237
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complement (18402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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CDS

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bucke, C.O., Burrows, C., Cherevoen, I., Chilliamyorth, C., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Croin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Gobble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lanard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Suth, R., Squares, R., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.

Nature 419 (6906), 527-531 (2002)
KNPKFQRLRFQNLPKLTKTKREVMDSCYKSEHLVESRTTGETFLVKMYRKAVMRGMSK
LSTKALMVPRLDDEGNAVYTKDIGDLCIFLSKSEPFCVSLSSLPRMFFPNNVEYMDAD
EDGYFNLARSSIVGDLTRMGTGVYIPPQNIDN"
                                                                                                                                                                                                                                                                                                                                                          / LTAIN ALL TONG TONG THE WALL CHRRKSVILVRSPLLSNGLSSSIRQTPPCTII DAVPCGEDLGKLVIYNANAVHFTYLEKKVPLELVDNPMVTIGSSHGWVATLSQDDGILL LAVDDLNBARSSPEDENCWYAVKELGP QISFCRPAQARSWINFRI PLPPLYTLPHCQYQLVTWYSMSSSSPEDENCWYAVKELGP QISFCRPAQANSEWINFRIANIANIAN AND SKYWFSEKHOLFRIPGGGGHIASWDHKDKH KNPKRQKLRFQKLRFQKLRFAKRRAVWRGMSK LSTKALMVFRLDDBGNAVYTKDIGDLCIFLSKSEPFCVSLSSLPRMFFPNNVEYMDAD
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Hamlin,N., Pain,A., Berriman,B., Hall,N., Bowman,S., Churcher,C.,
Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDGYFNLARSSIVGDLTRMGTGVYIPPQNIDN"
complement (33024. .36242)
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. 0.81;
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                                                                                                                                                                  pir||T05237
similar to unknown protein"
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                                                                                                    .28720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23;
Pred. No.
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Plasmodium falciparum MAL4P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="gene_id:MWJ3.9"
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                                                                                                       complement (27620.
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Conservative 0;
                                                                                                                                                                                                                                    /codon_start=1
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AL034557.8 GI:23498126
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TITLE JOURNAL

FEATURES

COMMENT

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1 ESJAKKENLJENKLINA, VFGALHGALDEBARANA I QLDLJOH TI ULKARIA TARKENLJENKLINA, VFGALHGALDEBARANI QLDLJOH TI ULKARIA TI UKRUMI TARKEYEDYPOPY TCEWKESONNY FRANCOJEKOPS LITESKOCKOCHOKAGKP I KIGGGANNI I VPTYPDYPOPY TCEWKESONNY FRANCOJEKOPS LIKKORGAGGERKYCOLINRYDCKOTASGKHVFFED PLANGEREMAEDDECKLARGHIKADA LYNYTESTE GCOCGOGKKKRODATTNYTESTE CKDCOYS CAPPUNI DINOKLEPLKORKXTYTEI TSGGGGGGGKKKADATTNYTESTE KKRYKROATTNYTESTE KKRYKONDI KOGGOGGGGKKKADATTNYTESTE CKOCGOSGGGKKKYGDADINING TPYTRYTCTER CHOCGARCKYCOGGARCKAGGGTKGADON CYTARAULKLEFLINGDTRKSDWO TPYTRYTCTER TRUHFCKOLD I EGYGCDAGYTLAAULKLEFLINGDTREKS CGCFEKWYKOCKKEKBWEA TRUHFCKOLD I EGYGCDAGYTLAAULKLEFLINGDTREKCH SKOLD I EGYGCDAGYTLAAULKLEFLINGDTREKCH SKOLD I EGYGCDAGYTLAAULKLEFLINGDTREKCH SKOLD I EGYGCDAGGYTLAAULKLEFLINGDTREKCH SKOLD I EGYGCDAGGYTLAAULKLEFLINGDTREKCH SKOLD I EGYGCOARGWALDOT I EREFLINGTREKTH I KOND SYDKYNOSONGNESLEDFRKKOOLD I EEEFL YTTAHESETKNI ETQDDIRGAATTAAAULKLEFLINGTREKEN GEGGTSOG WGGS TOTTPODWWQTY GKOLD I EGYGCOARGANTATO SKOKK THEY COND SYCKCKOORGNEN LTD USSKIK FROT YAHKY SKOLD ALLOGYKUN KKCKOOLD I KOND SYDKYNOSONGNESLEDFAKROD LATD SKOK GGEGGTSOG WGGS LOVD ALGONGNESLEDFAKKOOLD ALSONGNEN LTD VAND PROPAPATTGONNOS GGSSBASSEGGGTSOG WGGS LOVD COND COCCONTON COCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDHYSDITSSESEYEEMDINDIYABRAPKYKTLIEVVLEPSGNNTTASGNNTTASGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I KLKKEEWEK I KKHYLEKNKEGDNDMKSSVRNFLEKFEHRPEFNKA I KPCKGLTQFES
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KKKTKSTI DLLRVI NI PKSDYDI PTKLSPNRY I PYTSGKYRGKRY TYLEGBSGTDSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLDDKQIILIRALIKRWLEYFLEDYNKIKHKISDCINNGEGNICKRDCQNKCNCVGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MVRTGĞGGGGGVDKDGIDHQSAKHLLDSIGKKVHDQVKNGADGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similar to Plasmodium falciparum variant-specific surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa) fasta scores: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEVCMĀĀKYEGOSINTHYTKHEHSNKDSPSQLCTVLARSFADIGDIVRGKDLFYGNT
YESARREKLENKLKEVFGKIHGGLSEEAKKKYQDGDGNYYQLREDWWTANRETVWKAI
Direct Submission
Submitted (24-FBB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                              CBIO 15A, UK
CBIO 15A, UK
CBIO 15A, UK
CBIO Oct 3, 2002 this sequence version replaced gi:5731897.
CBIO Oct 3, 2002 this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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FKNKGBDIRETFVKSAALETY PAWKRYNDDNKKAEEBELKSGTI PENFKROMYYTFADY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MGTGSSTPSVPKDVKNESHNSARNVLENIGIEIYNEEKKKVNGY
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KELMDKFATLOTDIOSDAIPTCVCEKSLADKVEKGCLRCGYGLGTVAPTVGLIGSVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (3006 aa)
                                     RKENEL FGTINHVKHTTINR FAKPARDDPLHINQLEL FHTWLDRHRINMCEKWINKEELLD
KLAEEWENETHSGATHPSDSNKTLATDVSIQI BIDMDNPKPINGFTINMDINVDTPTMDIM
EDDIYYDVNDHDTSTVDSNTMDVPSKVQI EMDVNTKLVKEKYPIADVWDI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVWKPKALBAAIAKAIAEGTADIAAAAEAAGKARGMEFVIKALKHFGVENFFPGICDT
VGKANLYSGQNNVYSGIDPTSDNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /_ore="similar to Plasmodium falciparum variant-specific
surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 as
fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
()
(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similar to Plasmodium falciparum rifin pfb0030C
SWALL:096112 (EMBL:AE001367) (370 aa) fasta scores:
3.4e-65, 53.6% id in 375 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: PFD0020c"
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                                                                                                                                                                                                                                                                                                                                                                                                                upstream VAR gene PFD0005w"
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gene

CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEYPGEKYCGGDGHDCTENGELKHTNMFADLDCRDCHKQCRKYRKWIDIKFEEYEKQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKTDI CKLKNFNDKI DLNQYTTFKVFLEYWLQDF I EGYY I LKKRKI I EQCKENGGETC
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Matches 23; Conservative 0; Mismatches 22 AAGATGAAGAATGGTTTGATAAT 44

137861 AAGATGAAGAATGGTTTGATAAT 137839 셤 ઠ

AF288639S1 781 bp DNA linear PRI 06-SEP-2001 Homo sapiens glycine decarboxylase P-protein gene, exons 6 and 7. AF288639 AF288639.1 GI:15099927 of 6 AF288639S1 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

 (bases 1 to 781) Homo sapiens (human) Homo sapiens

Applegarth, D.A., Toone, J.R. and Coulter-Mackie, M.B.
Two novel mutations in the glycine decarboxylase (P-protein) gene
in patients with nonketotic hyperglycinemia (NKH) (Abstract)
Sist Annual Meeting of The American Society of Human Genetics 2001) In press AUTHORS TITLE REFERENCE JOURNAL

2 (bases 1 to 781) Toone, J.R., Applegarth, D.A. and Coulter-Mackie, M.B. Molecular investigations of nonketotic hyperglycinemia REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

AUTHORS TITLE JOURNAL REFERENCE

Unpublished

3 (bases 1 to 781)

5 Toone, Jr. A. Applegarth, D.A. and Coulter-Mackie, M.B.

1 Loose, J.R., Applegarth, D.A. and Coulter-Mackie, M.B.

2 Submitted (20-JUL-2000) Pediatrics, University of British Columbia, 4480 Oak St., Vancouver, BC V6H 3V4, Canada

3 Toone, J.R., Applegarth, D.A. and Coulter-Mackie, M.B.

4 (bases 1 to 781)

5 Toone, J.R., Applegarth, D.A. and Coulter-Mackie, M.B.

5 Toone, J.R., Applegarth, D.A. and Coulter-Mackie, M.B.

5 Toone, J.R., Applegarth, D.A. and Coulter-Mackie, M.B.

6 Toone, J.R., Vancouver, BC V6H 3V4, Canada

7 Amino acid sequence updated by submitter

7 Location/Qualifiers 181. .7 REMARK FEATURES

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669 350 CCTTGCTGCTACTTTTTCTGT 371 678 CCTTGCTGCTACTTTTTTCTGT 셤 ਨੇ

RESULT 10 BC045517 LOCUS

BC045517 1996 bp mRNA linear VRT 07-OCT-2003 Danio rerio mRNA similar to RIKEN cDNA 0610011F06 gene (cDNA clone MGC:56719 IMAGE:2601210), complete cds. DEFINITION ACCESSION

BC045517.1 GI:28278021

Danio rerio (zebrafish) VERSION KEYWORDS SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. Danio rerio

REFERENCE AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Wans, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butferfield, Y.S., Krzywinsk, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length

TITLE

human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 22388257

(bases 1 to 1996) 2477932 JOURNAL MEDLINE PUBMED

Strausberg, R. Direct Submission REFERENCE AUTHORS TITLE JOURNAL

Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

NIH-MGC Project URL: http://mgc.nci.nih.gov REMARK COMMENT

Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissaue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
Tissaue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 101 Row: d Column: 14

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Gaps

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Waterston, R.H.
Direct Submitsation
Submitted (12-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. The true order of the pleces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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HTG; HTGS PHASE1.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Peloderinae; Caenorhabditis.
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3;
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Waterston, R.H.
The sequence of Caehorhabditis elegans clone Unpublished
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1.8%; Score 22; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches (
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100.0%; Pred. No. 3;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 22; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKA FPNITWOPSEVETGSLSSIEAYROYHRLONVOPPIYLDVSGSWOTWGGFPAESCD
LIININWHISPLACTTGLFHGVGQILKPQGLLLTYGPYAFNGSIVPOSNFDFDQSLR
YRNPEWGLRDASFLTTLGQENGLRLEEIVDWPANNKCLLFRKDSVV"
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                                                                                                                   1.1996
| Crganism="Danio rerio"
| Crganism="Danio rerio"
| mol type="mRNA"
| farain="AB"
| db xref="taxon:7955"
| clone="MGC:56719 IMAGE:2601210"
| frissue type="Whole body, adult, (one male and one female, including unfertilized eggs)"
| clone lib="Sugano Kawakami zebrafish DRA"
| clone lib="Sugano Kawakami zebrafish DRA"
| clone lib="Sugano Kawakami zebrafish DRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MLNAAAADRNKDPILSVLKSRVASNRRLFALEISSGTGQHVVHF
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2 Lang, G.W., Sun, X.Y., Song, H.D., Zhou, Y., Liu, T.X.,
2 Lang, G.W., Sun, X.J., Wu, X.Y., Song, H.D., Zhou, Y., Liu, T.X.,
Deng, M., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y.,
Zon, L., Kanki, J.P., Look, A.T. and Chen, Z.
Deng, M., Sunki, J.P., Look, A.T. and Chen, Z.
Sun, Ecc. S.B. 2003) State Key Lab for Medical Genomics,
Submitted (Loc. SEP-2003) State Key Lab for Medical Genomics,
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University, 197 Rui Jin Road II, Shanghai
200025, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cypriniformes; Cyprinidae; Danio.

(Cypriniformes; Cyprinidae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="COG0220; Region: Predicted
S-adenosylmethionine-dependent methyltransferase [General
function prediction only]"
/db_xref="CDD:COG0220"
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            This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Similar to RIKEN cDNA 0610011F06 gene"
/protein id="AAH45517.1"
/db_xref="G1:28278022"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pME18S-FL3"
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/mol_type="mRNA"
/db_xref="taxon:7955"
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Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE INDEX.html) and The C. elegans ORFeome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans researchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
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4540. .4668,5201. .5444,5848. .5928,6033. .6111,7230. .7349))
/gene="Y45G5AM.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.wormbase.org/db/seq/sequence?name=Y45G5AM;class=Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Sequencing Center
Department of Genetics, Washington University
St. Louis , MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: submissions@watson.wustl.edu and jes@sanger.ac.uk
Submitted (24-JAN-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                              Waterston, R.
Direct Submission
Submitted (07-APR-2003) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, NO 63110, USA
                                                                                                                                                                                                                                                                                                 Submitted (04-OCT-2003) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For a graphical representation of this clone sequence and its
                                                                                                                                                                                                                                                                                                                                                     Louis, MO 63110, USA
On Nov 16, 2001 this sequence version replaced gi:15487595
Submitted by:
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/mol_type="genomic DNA"
/strain="Bristol N2"
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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
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University, Genome Sequencing Center, 4444 Forest Park Avenue, St.
Louis, MO 63110, USA
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University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
5 (bases 1 to 46826)
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Submitted (07-SEP-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                      AC084155
Caenorhabditis elegans cosmid Y45G5AM, complete sequence.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 46826)
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He sequence of C. elegans cosmid Y45G5AM
Unpublished (2001)
3 (bases 1 to 46826)
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AC084155.3 GI:16950482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-DEC-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA

11 (bases 1 to 83297)
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10 (bases 1 to 83297)
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Submitted (03-NOV-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
8 (bases 1 to 83297)
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Submitted (05-OCT-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
7 (bases 1 to 83297)
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Submitted (G1-AUG-2001) Department of Genetics, Washington
Submitted (G1-AUG-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
5 (bases 1 to 83297)
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                                                                                                                              Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
           Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                           Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                      2 (bases 1 to 83297)
Bradshaw-Cordum,H., Scott,K. and Graves,T.
The sequence of C. elegans cosmid Y71F9B
Unpublished (2001)
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Submitted (25-FEB-2000)
University, 4444 Forest
4 (bases 1 to 83297)
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Waterston, R.
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SDEGPIKLAAKTWSPDAVHITDSGINQFLKWALNGKSVPGFRQALLWCRRQADKFAMI
RGIQVRQWDKAFEEEAAGFCGDFERVCGRGDCLQIYSLIDSFESLTLSIMDDRISIYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(21980. .24877)
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COMMENT

ACO24201 Caenorhabditis elegans cosmid Y71F9B, complete sequence.

AC024201 AC024201.1 GI:7105616

LOCUS DEFINITION ACCESSION VERSION

RESULT 14 AC024201

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Genome Sequencing Center Department of Genetics, Washington University St. Louis , MO 63110, USA, and

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Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
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IICE: This sequence may not be the entire insert of this clone. may be shorter because we only sequence overlapping sections se, or longer because we provide a small overlap between neighboring submissions.

CDS

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

analysis see: http://www.wormbase.org/db/seq/sequence?name=Y71F9B;class=Sequence a graphical representation of this cosmid sequence and its

NEIGHBORING COSMID INFORMATION

The 5' cosmid is F32B5, 600 bp overlap; the 3' cosmid is W03D8, 300 bp overlap

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefindar (P. Green and L. Hillier, personal communication), the large scale EST projects of Vuji Kohara (Communication), the (http://www.ddbj.nig.ac.ip/c-elegans/html/CE INDEX.html) and The C. similarity to other profess from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions, and personal communications with C. elegans esearchers. tRNAs are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).

gene

CDS

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VCEQVKADCFSILEEFGIGWPEPLNCAQFPDPPELCMKPTEDBITGGFSAPRLPTKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains similarity to Pfam domains PF01392 (Fz domain), PF01534 (Frizzled/Smocthened family membrane region); coded for by the following C. elegans CDNAs: yk10907.5, yk150f10.5, yk241b7.5, yk269h10.3, yk275f4.3, yk275f4.3, yk275f4.3, yk341a1.3, yk31a11.5, yk496g4.3, yk494d1.5, yk496g4.5, yk512h12.3, yk512h12.5, yk513d5.3, yk512d5.5, yk513d5.3, yk513d5.5, yk513d5.5
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10848. .10957,12260. .12481,12529. .12817,13137. .13463,
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/protein id="Abf36028.1"
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/mol_type="genomic DNA"
/mstain="Bristol N2"
/db_xref="taxon:6239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Y71F9B"
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ALFSFLTFAIDRKRFRFPERCVFYLSLCIFISSLPYLTPLFIDAPIRSCHALGRGRSY
LSIGTFDNSYCLASFLLNYFFSTAAALWWLMFSFTLYLSGGRKWVPEGIEACSSYVHF
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SSSSKPTGCPSDLVDVDPHDPKSHCAFACQSNVMFSTDNKRMVRSWSIWFAAANAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (join(16537. .16738,17513. .17676,19079. .19399,
19849. .19878))
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15639. .15754)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to Pfam domain PF00226 prokaryotic heat shock prototain; coded for by the following C. elegans cDNAs: yk620a12.3, yk563e4.3, yk114h5.5, yk563e4.5, yk620a12.5"
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis. 1 (bases I to 83297) Waterston, R.H. REFERENCE AUTHORS

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TITLE The sequence of Caehorhabditis elegans clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 83297)
AUTHORS Waterston, R.H.

AUTHORS Waterston, R.H.

JOURNAL Submitted (01-MAR-2000) Genome Sequencing Center, Washington
JOURNAL Submitted (10-MAR-2000) Genome Sequencing Center, Washington
JOURNAL Location/Qualifiers

MO 63108, USA
Location/Qualifiers

1.083297

Author Author Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
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12 BM715133 13 BW045345 14 CR8989152 14 CR889801 29 CC826938 13 BM65845 13 BM65845 13 BM65845 13 BM65845 14 CD268604 14 CD268604 15 BM72895 16 BM3316 17 BM283578 18 BW281378 19 BW281378 11 BM281378 11 BM281378 11 BM281378 12 BM311239 13 BW281359 14 CD267519 14 CD267519 15 BM281354 16 BM311239 17 BM28139 18 BM28139 18 BM28139 19 BM28139 11 BM28139 11 BM28139 11 BM28139 12 BM28139 13 BM28139 14 CF674636 15 BM2839 16 BM881639 17 CF77636 18 BM283644 18 BM283644 19 BM283644 10 BM617656 11 BM283644 11 CF777891 14 CF777891 14 CF777891 14 CF777891 14 CF777891 14 CF777891 15 BM283644 16 CF777891 17 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891 18 CF777891	6 7 Arabidopsi 1.19877675 aliana (thal aliana (thal aliana (thal aliana (thal aliana (thal aliana, isans 68 II; Brass 645) aka,M., Ishi Ayashizaki, alysis of Anakayashizaki, alysis of Aik ki Seki
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Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                   H76984 1708 SST 05-JAN-1998 TH 15 Lambda-PRL2 Arabidopsis thaliana cDNA clone 200N2T7, mRNA
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/clone_libe_Liambda-PRL2"
/clone_wetcor: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1)
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
grown roots; 3) staged plants half with 24 hour light
grown roots; 3) staged plants half with 24 hour light
grown roots; 3) staged plants as 3 but aerial tissue (stems, flowers and
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.
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MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
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14.3%; Score 175; DB 14; Length 589;
Best Local Similarity 99.6%; Pred. No. 2e-79;
Matches 225; Conservative 0; Mismatches 1; Indels
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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                                                                                                                                                    AU229698

AU229698 RAFL17 Arabidopsis thaliana cDNA clone RAFL17-32-017 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. rhis clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Seki, M., Narueaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Miraha, Y., Bahi, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K. Barge scale analysis of Arabidopsis full-length cDNA
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                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   819 AGGTTTCTTTAGGAGCCATAGGGATTGTGTTTTGTGCATCATCACTAGCTTCTGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
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/lab_host="DH108"
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Best Local Similarity 100.
Matches 242; Conservative
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BH601144.1 GI:17853590
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Fax: 301-838-0208
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BH601144
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                                                                                       807 bp DNA linear GSS 16-DEC-2002
BONFA70TF BO 1.6 2 KB tot Brassica oleracea genomic clone BONFA70,
PSS01737
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Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 395)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                     Brassica oleracea
Wharyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida <u>I</u>I; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="BO 1.6 2 KB tot"
/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea (Dupublished (2001)
Other GSSs: BONFA70TR
Contact: Chris Town
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Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
SQA primer: TF
Class: sheared ends.
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9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
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/organism="Brassica oleracea"

/mol type="genomic DNA"

/strain="TO1000DH3"

/db xref="taxon:3712"

/clone="BONFA70"
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                                                                                                                                                                                                                   GSS
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BZ501737/c
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BH601144 784 bp DNA linear GSS 15-DEC-2001 BOHJF33TF BOHJ Brassica oleracea genomic clone BOHJF33, genomic
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Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (Dases I to 784).
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Ombublished (2001)
Other GSSs: BOHJF33TR
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
This is single pass sequence Constant Canal 
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/clone="BOHJF33"
/clone="bDHJF33"
/clone="bDHJF31, site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Org primer: IF
Class: sheared ends.
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/organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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AUTHORS TITLE JOURNAL COMMENT

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BH657185

BOMGR19F BO_2 3 KB Brassica oleracea genomic clone BOMGR19, genomic survey sequence.
BH657185
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            93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infoblogen.fr).
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                              Length 227;
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                                                                                                                                                                                             /organism="Brassica napus"
/mol_type="mkNA"
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/db_xref="taxon:3708"
/db_xref="restored"
/tissue_type="anthers"
/clone_lib="RRO2"
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0.0019;
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/clone="BOMGP19"
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Class: sheared ends.
Location/Qualifiers
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Matches 26; Conserv
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BH657185
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RFO2.120J16F010607 RFO2 Brassica napus CDNA clone RFO2120J16, mRNA
sequence.
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RFO2.125P19F010622 RFO2 Brassica napus CDNA clone RFO2125P19, mRNA
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Eukaryota inpus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 (bases 1 to 227)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
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Location/Qualifiers
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            Query Match 2.5%; Score 31; DB 28; Length 784; Best Local Similarity 100.0%; Pred. No. 0.00027; Matches 31; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.0019;
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                       65 CTATAGGAACATGTGGAGGTCCTTTGTTAAC 95
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Brassica napus
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RESULT 8 CD842095

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REFERENCE AUTHORS TITLE JOURNAL COMMENT

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BH601155 82 15-DEC-2001
BOHJF33TR BOHJ Brassica oleracea genomic clone BOHJF33, genomic
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 824)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whoule genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                /.organism="Brassica oleracea"
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/db_xref="Heaxon:3712"
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/clone="BONFA70"
/note="borcor: pH051; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pH051 using BstXI linkers"
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared-
genomic DNA inserted into pHOS1 using BstXI linkers"
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Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
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/db xref="taxon:3712"
/clone="BOHJF33"
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Fred. No. 0.11; hes 26; Conservative 0; Mismatches
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Matches 26; Conservative
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BONFA10TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONFA70, genomic survey sequence.
BZ501745.1 GI:27018772
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1 (bases 1 to 761)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Other GSSS: BONFA70TF
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Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roslids; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 728)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nabh,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shoty reads from Brassica oleracea
                                                                         BZ050387 11near GSS 09-OCT-2002 jnr42f08.g1 B.oleracea001 Brassica oleracea genomic, genomic survey
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2.1%; Score 26; DB 28; Length 728;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K. Wilson
Contact: Richard K. Wilson
Genome Sequencing Center
Genome Sequencing Center
Email: submissions@watson.wustl.edu
Email: submissions@watson.wustl.edu
Plate: jnr42 row: f column: 08
Seq primer: -28RPPOT reverse
Class: shotgun
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High quality sequence stop: 202.
Location/Qualifiers
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COMMENT
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                                                                                                                                                         ACCESSION
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KEYWORDS
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Gaps

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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 03-NOV-2001
                  Eukaryofe, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (base 1 to 445)
Alonso,J.W., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Shinn,P., Zimmerman,J. and Ecker,J.R.

Asquence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG078331 1082 bp DNA linear GSS 03-NOV-2003
Pan troglodytes DNA, clone: PTB-073J18.F, genomic survey sequence.
AG078331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db kref="taxon:3702"
/clone="SALK_011524"
/clone="SALK_011524"
/clone="Dis="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used car be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Direct Submission
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA FILE 1888 453 4100 x1752 Fax: 858 558 658 659 Email: ecker@salk.edu
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/mol_type="genomic DNA"
/strain="Columbia 0"
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Conservative 0; Mismatches
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Pan troglodytes
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401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3689

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 9002 row: C column: 21

Seg primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
ECORI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
                                                                                                   GSS 10-NOV-1999
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                           Q901299 737 bp DNA linear GSS 10-NOV-S_5234_AL B11_T7A RPCI-11 Human Male BAC Library Homo sapiens enomic clone Plate=9002 Col=21 Row=C, genomic survey sequence.
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1 (bases 1 to 737)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell.S., Holms
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100.0%; Pred. No. 1.2;
tive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="Plate=9002_Col=21_Row=C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                                                                                                                                                    Homo sapiens (human)
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BH251397
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                                          RESULT 13
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Sequencing: -21M13
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Vector : pKS145
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Search completed: September 25, 2004, 14:17:27 Job time : 3727 secs

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September 25, 2004, 06:59:56; Search time 548 Seconds (without alignments) 9496.428 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaa97919 A: thalia	Aac44184 Arabidons		Aac36831 Arabidops	4	Aaa97925 A. thalia	Aaa97924 A. thalia	Aac46395 Arabidops	Aac39779 Arabidops			Abz14407 Arabidops		Ada70627 Rice gene	Abn85767 Arabidops	Aaa97923 A. thalia	Ada70213 Rice gene	Aaa97921 A. thalia	Aac51119 Arabidops	Aac37289 Arabidops	Ada70748 Rice gene	Ada69686 Rice gene	Ada69568 Rice gene
SUMMARIES	ΙD	AAA97919	AAC44184	AAA97920	AAC36831	AAC47974	AAA97925	AAA97924	AAC46395	AAC39779	AAC37652	AAA97922	AB214407	ADA68246	ADA70627	ABN85767	AAA97923	ADA70213	AAA97921	AAC51119	AAC37289	ADA70748	ADA69686	ADA69568
	DB		m	m	m	m	ო	ო	ო	m	m	٣	9	^	7	9	ო	7	ო	ო	٣	7	7	7
	Query Match Length	1225	2586	1049	493	2660	101	1081	1418	1421	1403	1293	3387	3387	1200	83698	1194	1152	1145	1292	1295	2175	1155	1040
· dr	Query Match	9.66	73:6	42.7	36.8	11.7	11.5	11.1	10.8	10.7	10.5	10.4	10.4	10.4	10.1	9.6	9.3	8.5	7.6	7.6	7.5	7.1	6.7	6.1
	Score	1220.2	901.2	523.2	450.6	143.6	140.6	135.8	132.8	131.2	128.8	127.2	127.2	127.2	123.4	117.2	113.4	103.8	93.2	93.2	91.6	86.8	82	74.2
	Result No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23

Abx56692 Arabidons		Human		Abl32105 Human imm	Abz15497 Arabidops	Ada71938 Rice gene	Aas46530 Tumour su		Abl34476 Human met	Abl70513 Chemicall	_	Abk33960 Human DNA	Ada20357 Prostate	Ada84164 Human ren	Adb54090 Pretreate	Adb54218 Pretreate	Ade84080 Human lym	Ade84156 Human lym	Abl34435 Human imm	Abl34460 Human met	Abl34430 Human imm
ABX56692	ABQ67093	ABL33959	ABK39921	ABL32105	AB215497	ADA71938	AAS46530	ABL32362	ABL34476	ABL70513	ABL32232	ABK33960	ADA20357	ADA84164	ADB54090	ADB54218	ADE84080	ADE84156	ABL34435	ABL34460	ABL34430
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55	49	48	47.2	47.2	45.6	45.6	45.6	45.6	45.6	45.6	45.2	45.2	45.2	45.2	45.2	45.2	45.2	45.2	45.2	45	45
24	25	26	27	28	c 29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAA97919 standard; DNA; 1225 BP.

RESULT 1

AAA97919

Nucleic acid, useful for producing transgenic plants with altered nucleobase transport, encodes a nucleobase transporter protein of Arabidopsis thaliana. PUP1; transgenic plant; nucleobase transporter; apical dominance; flowering behaviour; senescence; pesticide distribution; ds. Frommer WB; Andre B, Location/Qualifiers /*tag= a /product= "PUP1" 99DE-01007209. 99DE-01007209. 19-JAN-2001 (first entry) 25. .1095 /*tag≕ a Gillissen B, Buerkle L, A. thaliana PUP1 DNA #1. Arabidopsis thaliana. WPI; 2000-566202/53. (FROM/) FROMMER W. P-PSDB; AAB10684 DE19907209-A1 19-FEB-1999; 19-FEB-1999; 24-AUG-2000 AAA97919; Key

Claim 2; Page 11; 24pp; German.

This invention describes a novel nucleic acid encoding a plant nucleobase transporter (1). (1) is produced by complementation of a nucleobase transport (NBT)-defective host cell with a plant gene bank by selection of NBT-positive celle. (1) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the

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841 GGGATTGTGTTTTGTGCATCATCACTAGCTTCTGGTGTTCTGATAAGTGTTCTGCTTCCG 900
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29-MAR-1999;
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16-APR-1999;
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28-APR-1999;
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14-MAY-1999;
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     encoded protein (II) in prokaryotic or eukaryotic cells, for inhibiting expression of (II) (when in antisense orientation), and to produce transgenic crop plants. The transgenic plants have modified nucleobase transport properties, e.g. altered affinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in a pical dominance, flowering behaviour and senescence, or improved distribution of pesticides. This sequence encodes the Arabidopsis thaliana PUP1 protein which is described in the method of the invention
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                                                                                                      Score 1220.2; DB 3; Length 1225; Pred. No. 0; 0; Mismatches 3; Indels 0;
                                                                                     Sequence 1225 BP; 309 A; 252 C; 261 G; 403 T; 0 U; 0 Other;
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Best Local Similarity 99.8
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                    TCTCTACTTCTTTTTTTTGGGGATTTGTCTTTACTTCTACGGCGAGTTTAAATCCGGC
                                                                                                                                                                                        AAGAAAGTTGTTGATAAACCTCAACCGCCGGAGACAGAACTGCCTATTCTTCCAGTTAGT
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This invention describes a novel nucleic acid encoding a plant nucleobase transporter (I). (I) is produced by complementation of a nucleobase transport (NBT)-defective host cell with a plant gene bank by selection of NBT-positive cells. (I) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the encoded protein (II) in prokaryotic or eukaryotic cells, for inhibiting expression of (II) (when in antisense orientation), and to produce transpenic crop plants. The transgenic plants have modified nucleobase transport properties, e.g. altered affinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in apical dominance, flowering behaviour and senescence, or improved distribution of pesticides. This sequence encodes the Arabidopsis thaliana PUPI protein which is described in the method of the invention
2487 GAGCAITACTGTTATGTTTTGTTCCT-AATATTATGTGTGATTGTGTG-TTTTGTTATTG 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGATGAAGATGAAGACAGTTCTTGTAATCATAAACTGTATATTCTTGGCCATTGGAAAC
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                                                                                                                                                                                                                                                           PUD1, transgenic plant; nucleobase transporter; apical dominance;
flowering behaviour; senescence; pesticide distribution; ds.
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                                  TTCTTGTGTATAAGTATGAATAAATTTGAAAGATATTGAGC 1224
                                                  Frommer
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                                                 ATAATCGGAACTCAACTATCAACGCTCTCTTCGCTTTCTTGTTAGTCAAGCAAAG
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Pred. No. 1.9e-114;
); Mismatches 4;
9908-015363P.
9908-0153070P.
9908-0154018P.
9908-0154018P.
9908-015403P.
9908-015513P.
9908-015513P.
9908-015563P.
9908-015659P.
9908-015659P.
9908-0157753P.
9908-0157753P.
9908-0157753P.
9908-0157753P.
9908-0157753P.
9908-015823P.
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9908-015823P.
9908-015823P.
9908-015923P.
9908-015963P.
9908-015963P.
9908-01696P.
9908-01696P.
9908-01696P.
9908-01608P.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.8%;
Best Local Similarity 99.1%;
Matches 453; Conservative
 10-SEP-1999;

110-SEP-1999;

110-SEP-1999;

110-SEP-1999;

120-SEP-1999;

220-SEP-1999;

24-SEP-1999;

24-SEP-1999;

24-SEP-1999;

26-OCT-1999;

13-OCT-1999;

13-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

14-OCT-1999;

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16-OCT-1999;

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27-OCT-1999;

28-OCT-1999;

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28-OCT-1999;
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21 - JUN - 1999;
22 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
28 - JUN - 1999;
29 - JUN - 1999;
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18-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
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02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
TCAACTICATCGCTCATAATCGGAACTCAACTAGCTITCAACGCTCTCTTCGCTTTCTTG 420
                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 55799.
                                                                                                                                          AAC47974 standard; DNA; 2660 BP
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0121825P

99US-0123180P

99US-0126248P

99US-0126248P

99US-0126248P

99US-0126248P

99US-0126785P

99US-0128714P

99US-0130077P

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99US-0132481P

99US-0134218P

99US-0134218P
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99US-0138540P
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                                                                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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08-JUN-1999;
10-JUN-1999;
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                                                                                                                                                                                                                                                                                                              768 AGGATCAGTGTTTACTATGCATTGATAGTGATCACAGGAATAATAGTGGCAAGGTTTCTT
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                                                                                                     GTTGACGGTTGGTATCGGGATCCTTGCGTTACACAGTGATGGAGACAAACCGGCTAAGGA
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418 CTATGTTTTGCTCGGTGTGATCATTGCTGGAGATAATATGTTATACTCTGTTGGACTTTT
                                                           GAGCAAGAAAGAGTATGTGGTTGTGTTCTTGATGACTGTGTGCAGCTCTTCTGTATGC
                             598 cridricaricrececrecritaaradcrercaareardardeedaracricricregrer
                    348 ATATCTGCCAGTTTCAACTTCATCGCTCATAATCGGAACTCAACTAGCTTTCAACGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 5.1e-29;
0; Mismatches 374; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                      9905-0157865P

9905-015823P

9905-015823P

9905-015823P

9905-015929P

9905-015929P

9905-015923P

9905-015933P

9905-015933P

9905-015933P

9905-015938P

9905-015963P

9905-01607P

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9905-01607P

9905-01609P

9905-01609P
                                                                                                                                                                                          9908-0151080P-
9908-0151303P-
9908-0151330P-
9908-0152363P-
9908-0153070P-
9908-0154018P-
9908-0154018P-
9908-0154039P-
9908-0154039P-
9908-0155139P-
9908-0155486P-
9908-0155689P-
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99US-0157117P.
99US-0157753P.
              99US-0148171P.
99US-0148341P.
99US-0148365F.
99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149722P.
99US-0149722P.
99US-0149723P.
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|larity 50.3%;
|Conservative
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Best Local Simi:
Matches 381;
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07-0CT-1999)
12-0CT-1999)
13-0CT-1999)
13-0CT-1999)
14-0CT-1999)
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14-0CT-1999)
121-0CT-1999)
21-0CT-1999)
21-0CT-1999)
21-0CT-1999)
22-0CT-1999)
22-0CT-1999)
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13-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
24-SEP-1999;
24-SEP-1999;
28-SEP-1999;
28-SEP-1999;
04-OCT-1999;
05-OCT-1999;
                                                                                                                                                    25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
                           11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
                                                                                                                       20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
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99DE-01007209. 99DE-01007209

19-FEB-1999; 19-FEB-1999;

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3; Gaps

CICCAIDGICAIAGGGITGCICACAGGACITGACAACIACITATATICITACGGAITAGC 347

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Andre B,
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                                                                                                                                                                                                                                                                               AAA97924 standard; DNA; 1081 BP.
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                                                                                                                                                                             CTICCAG 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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                                                                                                                   1009
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                                                                                                                                                                                                                                                                                 This invention describes a novel nucleic acid encoding a plant nucleobase transporter (1). (1) is produced by complementation of a nucleobase transport (MBT)-defective host cell with a plant gene bank by selection of NBT-positive cells. (1) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the encoded protein (11) in prokaryotic or eukaryotic cells, for inhibiting expression of (II) (when in antisense orientation), and to produce transport crop plants. The transpenic plants have modified nucleobase transport properties, e.g. altered affinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in apical dominance, flowering behaviour and senescence, or improved distribution of pesticides. This sequence encodes the Arabidopsis thaliana PUPI protein which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 TCCATTGTCATAGGGTTGCTCACAGGACTTGACAACTACTTATATTATTACGGATTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCTACCTGTTTCTACCCTTTCCCTGATCTGCATCACAGTTAGCCTTCACGCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTTATAAATATGATAATCTACATGAGTCTAGTGGCCAGTTGTGTTAGCGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTTCATCGTTGGAGATTTTAAGGTGATAGCAAGAGAAGCAAGAGGTTCAAGATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 CTTTTTGCTAGTAGCGAGTGGAAACTTTGAGCAGTGAAATGGAAAACTACAAACTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGGAGCCATAGGGATTGTGTTTTTGTGCATCATCACTAGCTTCTGGTGTTCTGATAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITATATATACCGCTCGTTGAGCTAACTTACAAGAAAGCTCGTCAAGAAATCACTTTCCCA
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                                                                                                 Nucleic acid, useful for producing transgenic plants with altered nucleobase transport, encodes a nucleobase transporter protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1071;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1071 BP; 307 A; 236 C; 208 G; 320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 394; Indels
                                            Frommer WB;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 140.6; DB 3
Pred. No. 2.3e-28;
                                            Andre B,
                                                                                                                                                         Claim 2; Page 15; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
                                          Buerkle L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 390; Conservative
                                                                                                                               Arabidopsis thaliana.
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                                                                     WPI; 2000-566202/53
                                         Gillissen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               958 TATCTTGATGAAACAAACTTGAAGAAAGTAATGAAATACCAACAACAGAATCCCCTGAC 1017
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                                                                                                                                                                                                                                                                      898 Traaaggrgarricrargarricragcrarricgegerricgrarccrargrcraccaacaa 957
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838 TIGGGACTCCCCGTGGTTCCTATCCTGGCTGTCATCATTTTCCATGACAAAATGAACGGC
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09-MAR-1999;
23-MAR-1999;
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Pred. No. 1.1e-25;
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       Hybridisation assay; genetic mapping; gene expression control; protein identification; asgnal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
              Arabidopsis thaliana DNA fragment SEQ ID NO: 18172.
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                                        AGTICAAGATTGGAGGATCAGTGTTTTACTATGCATTGATAGTGATCACAGGAATAATAT 814
               CTCTTCTCTATGCTTTTATATTACCGCTCGTTGAGCTAACTTACAAGAAAGCTCGTCAAG 634
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                             This invention describes a novel nucleic acid encoding a plant nucleobase transporter [1]. (I) is produced by complementation of a nucleobase transport (NBT)-defective host cell with a plant gene bank by selection of NBT-positive cells. (I) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the encoded protein (II) in prokaryotic or eukaryotic cells, for inhibiting expression of [II] (when in antisense orientation), and to produce transgenic crop plants. The transgenic plants have modified nucleobase transport properties, e.g. altered affinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in apical dominance, flowering behaviour and senescence, or improved distribution of pesticides. This sequence encodes the Arabidopsis thaliana PUP1 protein which is described in the method of the invention
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Pred. No. 1.3e-24;
0; Mismatches 418; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1293 BP; 345 A; 288 C; 247 G; 413 T; 0 U; 0 Other;
1f; Page 13; 24pp; German
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Matches 391; Conservative
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) array or probes representative of the plant cell genome; and (b) characteristic of a stress response. The method is useful in the characteristic of a stress response. The method is useful in the plants production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abicic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (AB212196-AB217574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      495
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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Pred. No. 2e-24;
0; Mismatches 418; Indels 3;
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SYNGENTA PARTICIPATIONS
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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Hou Y; I, Zou Ļ SA, Zhu Goff B Z,

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Glazebrook Whitham S,

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Chang H, Chen W, Coc Katagiri F, Quan S,

(SYGN) SYNGENTA PARTICIPATIONS AG.

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                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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                                                   Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 cerecirces as de consecuences de consecuences de consecuences de consecuences de consecuencia de consecuen
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                                                                                            TCTIACITICIACGGCGAGTITAAATCCGGCAAGAAAGTTGTTGATAAACCTCAACCGCCG 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 CTTCCTCATGGAAACTCCTCTGTGGAGCGCCTCCATTGTCATAGGGTTGCTCACAGGACT
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Pred. No. 1.4e-23;
0; Mismatches 396; Indels 27;
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T, Zou
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Xie
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Whitham S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYGN ) SYNGENTA PARTICIPATIONS AG
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Conservative C
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Katagiri F,
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569 557 629

The invention relates to an isolated nucleic acid molecule (I), maize yellow stripe 1 (ys1) or yellow stripe1-like (ys1) from Arabidopsis (ABN85763-ABN85771). (I) is useful for generating transgenic plants which can be used for enhancing iron uptake from soil and for bioremediation of metal or heavy metal contaminated soil. (I) may also be used to alter the distribution of iron within the plant body so that edible parts of crop plants have more iron. Transgenic plants may also be used in conventional plant breeding schemes to produce progeny which also contain the gene of interest. The present sequence is that of the Arabidopsis ysl encoding New yellow stripel and yellow stripel-like genes, useful for altering the distribution of iron within the plant body so that edible parts of crop plants have more iron, or for producing plants useful in enhancing iron uptake from soil. Claim 1; Page 114-159; 187pp; English Dellaporta WPI; 2002-490144/52 P-PSDB; ABB83920 Walker EL,

Sequence 83698 BP; 26295 A; 15150 C; 15104 G; 27149 T; 0 U; 0 Other;

Gaps DB 6; Length 83698; 3, Score 117.2; DB 6; Length Pred. No. 4.9e-21; 0; Mismatches 388; Indels Query Match
Best Local Similarity 48.1%;
Matches 363; Conservative

67442 Crcriscrrrrarcrrrrcrcrrscrrrrscrrrrscrrrrscarracarrarrrrrrraracr 67501 CTCTGTGGAGCGCCTCCATTGTCATAGGGTTGCTCACAGGACTTGACAACTACTTATATT 275

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CTTACGGATTAGCATATCTGCCAGTTTCAACTTCATCGCTCATAATCGGAACTCAACTAG crerresacritrararcrecerresacritaricarrerargementare 335 67502

CTTTCAATGGTGTCTTCTATTATTACATCAATTCTCAGAAATCACTTGTTTGATTTTCT 67621 455 ACGCCGTCGTTTGTTGACGGTTGGTATCGGGATCCTTGCGTTACACAGTGATGGAGACA 57562

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GCCAAGGTTTCTTCTTAGGAGCCATAGGGATTGTGTTTTGTGCATCATCACTAGCTTCTG 874 57922 Adrircag---GaadGrcaaGrcarrrangrrrrgacrrrgGrcgGgggggggrrrcgr 815

AGTICAAGATIGGAGGATCAGTGTTTTACTATGCATTGATAGTGATCACAGGAATAATAT

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68099 ACAAGCTGACTGAGGTTAAGATGGTGGCGATGCCCATCGCCTTCACAGGATTCACGTTTT 68158 994 995 ACTICIACGGCGAGITIAAAICCGGCAAGAAGI 68159 ATATCTACCAGAACTATCTTGATGACTTGAAAGT g 8 셤

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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- protein search, using sw model OM protein

September 23, 2004, 23:47:26 ; Search time 23.3672 Seconds Run on:

(without alignments) 777.685 Million cell updates/sec

Perfect score: Sequence:

US-09-913-767-9 1760 1 MYKALVIINCIILAIGNCGG......QQEESQETEQSSLSRPISEC 352

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

(Ggn2_6/ptodata/2/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/5B_COMB.pep:*
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(Ggn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/2/iaa/backfiles1.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 25058, A	7	~	59	25514,					4311,	5007		7304,	366		4	8	12578,	7510,		27266,	Sequence 28655, A	7512,		3732,	7791	524, A
SUMMAKIES	ID	US-09-252-991A-25058	US-09-024-848-2	US-09-348-116A-2	Α.	9-252-	÷	US-09-107-532A-4393	US-09-540-236-2922	US-09-489-039A-8024	US-09-543-681A-4311	9-328-	US-09-328-352-4442	9-328-352-73	US-09-134-001C-3948		US-08-898-976-4	0	US-09-489-039A-12578	9-543-	-13	US-09-252-991A-27266	US-09-252-991A-28655	٩	US-09-252-991A-19581	US-09-134-000C-3732	US-09-543-681A-7791	US-09-198-452A-524
	DB	4	7	m	4	4	4	4	4	4	4	4	4	4	4	7	~	4	4	4	4	4	4	4	4	4	4	4
	Query Match Length	327	292	292	494	464	514	867	296	325	405	469	730	434	503	462	462	940	414	424	297	303	445	449	720	394	421	465
de	Query	7.3	7.2	7.2	7.2	7.1	6.7	•	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.3	6.3	6.3	•	6.2	6.2	6.2	•	•	6.1	٠	6.1	6.1
	Score	129	126	126	126	125.5	118.5	118.5	114.5	114	114	112.5	112.5	112	112	110.5	110.5	110.5	110	109.5	109	108.5	108.5	107.5	107.5	107	107	107
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-328-352-5249	US-09-252-991A-28081	US-09-134-001C-4475	US-09-328-352-7092	US-09-328-352-7659	US-09-543-681A-5385	US-09-252-991A-19515	US-09-024-848-4	US-09-348-116A-4	US-09-543-681A-4421	US-09-252-991A-17668	US-09-134-000C-5653	US-09-134-001C-3001	US-09-489-039A-7419	US-09-107-532A-4163	US-09-543-681A-8204	US-09-068-195-24	US-09-328-352-4689
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106.5	106.5	106.5	106	105.5	105.5	105.5	103.5	103.5	103.5	103	103	102.5	102.5	102	101.5	101.5	101.5
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ALIGNMENTS

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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: 107136.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
RIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25058
LENGTH: 327
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                                                      Sequence 25058, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25058
JS-09-252-991A-25058
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RESULT 2 US-09-024-848-2 ; Sequence 2, Application US/09024848.

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137 ----IGGIIAQTYK-VEQVNSFYI-GILCALVCAIAWGSESVLSSFAMESELSEIEALLI 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 L----SGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFWVKHKFTPFTINAVVLLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 FSTFLETAGFPV-----IFIPLLFSYITRRESNNVGDSTSFFLIKPRLLIAAVIVGI 88
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          GENERAL INFORMATION:
APPLICANT: Lonetto, Michael A.
APPLICANT:
TITLE OF INVENTION: No. 5962295el LicB
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,848
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Patent No. 6200779
GENERAL INFORMATION:
APPLICANT: Lonetto, Michael A.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/033,807
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GMS0017
TELECOMMUNICATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 23.2
Matches 67; Conservative
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                                                                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                  ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                            USA
Patent No. 5962295
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
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Sequence 5990, Application US/09543681A

Sequence 5990, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION WINDER: 1050-001

CURRENT APPLICATION WINDER: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 L----SGFDNYLYAYGIAYLEVSTAALIIASQLAFIAIFSFFMVKHKFTPFTINAVVLLT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 LLAGPIGMQANLYA--VKYIGSSLASSVSAIYPAISVLLAFFFEKHKISKNTVFGIVLI- 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 7.2%; Score 126; DB 3; Length 292; Local Similarity 23.2%; Pred. No. 8.4e-05; nee 67; Conservative 55; Mismatches 99; Indels
               SEE: Dechert, Price & Rhoads
: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Disserte
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastERO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/348,116A
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/024,848
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: 60/033,80'
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFRENCE/DOCKET NUMBER: GMSO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-994-2222
CORRESPONDENCE ADDRESS: ADDRESS:
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US-09-348-116A-2
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US-09-543-681A-5990
                                                                                                                      USA
                                                                                                                   COUNTRY:
ZIP: 191
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Matches
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILTE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4255
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---EQIAHE 238
                                                                                                         196 KOTMSYTLVLEFQLILCLL-----ASIVSVIGMFIAGDFKQALPKEAREFKLGE---- 244
                                                                                                                                                                                           299 LYTFGYARGFELEKILRLIDQSLAPAAAIVMIIG--AGGGFKQMLVASGVGDVIGHLAVN 356
                                                                                                                                                                                                                                                                                     | ::| | ::| | ::| | 357 AQISPILLAWLVAAVIRIATGSATVATITGAGIVVPVIDLIPGVNRELLVLATGAGSLIL 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 FFFWEMMLIPMYFLISLWGHKGSSDEKHVSAATKFFIYTQASGLLMLLAIIGLAVAFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 ----PVHGWLADAHABAPTAGSVDLSGILLKTAAYGLLRFNLPLFP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 VLEFQLILCLLASIVSVIGMFIAG--DFKQA-LPKEAREFKLGEALFYVVAVF--SAIIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FLGAIGLIFSTSSL--
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                                                                                                                                                                                                                                                                                                                                                                                          417 SHVNDAGFWLVKQYFNMSVSĖTĖKTWTAMETILSVVGLV 455
       GKTILYGLIVALPTAAIAGPLFGALVSRYIPGTPSABLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.7%; Score 118.5; DB 4; Best Local Similarity 19.5%; Pred. No. 0.001; Matches 71; Conservative 49; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 PGTGNFVGEFMILFGTYGHFKLITIISVFGLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4255, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
                                                                        163 THKQYITGFLITVAAAVMYAFILPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 ETDKPVH----ETHKQY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Proteus mirabilis US-09-543-681A-4255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 QGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 IKSGE 327
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                              193
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 MIVLYGFFGLPQYGLVGVAWST---VVGRIIAVVL---LCGLLFYGLRIKFDIRL--L 273
                                                                                                                                                                                                                                                                                                                                                                                     89 LSGFDNYLYAY-GIAYLPVSTAALIIASQL--AFIAIFSFFMVXHKFTPFTINAVVLLTV 145
                                                                                                                                                                                                                                                                                                                                                                                                                 146 GAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAF----ILPLVELAYQKAKQTMSY 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFY------VVAVFS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AIIWQGFF----LGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLAL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --IPLLFSYITRRRSNNVGDSTSFFLIK---PRLLIAAVIVGILSGFDNYLYAYGIAYLP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 VSTA---ALIIASQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHE 162
                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                          ---IAAVIVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GAG-----KRDKASQAIHISIAFNFLLGFSSAIIILFFGYNILNVMNTPEHLVQDGYNY
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 125.5; DB 4; Length 464; 2.1%; Pred. No. 0.00018; Ve 51; Mismatches 139; Indels 121;
                                                                                                                                                                                                                                                         74;
                                                                                                                                                                                              Query Match 7.2%; Score 126; DB 4; Length 494; Best Local Similarity 22.8%; Pred. No. 0.00017; Matches 69; Conservative 57; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                              37 FSTFLETAGFPVIFIPLLFSYITRRS---NNVGDSTSFFLIKPRLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25514, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
       60/128,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
PRIOR APPLICATION NUMBER: US 6 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 SEQ ID NO 5990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.1%;
                                                                                                            TYPE: PRT; ORGANISM: Proteus mirabilis
US-09-543-681A-5990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.13
Matches 88; Conservative
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274 VIW 276
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US-09-252-991A-25514
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us-09-913-767-9.rai

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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARFAITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2922
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Sequence 8024, Application US/09489039A

Sequence 8024, Application US/09489039A

Figure No. 661089

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 2709-2004001

CURRENT PELLING NUMBER: US/09/489,039A

CURRENT PELLING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AG---DFKQALPKBAREFKLGEALFYVVAVFSAI----IWQGFFLGAIGLIFSTSSLVSG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 VGWTPIQPQMLP-----YLFGIGLFRAMIGQLSMTHAYKVGRKFMVSALGYLVVVLSMLYG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 RPSILGHGLLPTLIGLTSGAMAGYAYLQVRELSLLGEPSWRIVFYFAVLATLISAIASTV 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 VIGVYNLPDFPHRRHHFISFFLFPSEKİWFSGLLAİIAVSFMIVLFVHFLQGEKKQIGEA 523
408 YVLLSDFSFTPVVFLSILLLIILASKNELFREQLIYSWEWRTIDGIIIGALSLLY---1 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 QLAFIAIFSFFMVKHKFTFFTINAVVLLIVGAAVLGMHTETDKPVHETHKQYITGFLLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 AAAVMYAFILPIVELAYQKAKQTMSYTLVLEFQLI-------LCLLASIVSVIGMFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 296;
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                                           ---IMISVLLPITEV--LAVIFYH-
                                                                                                                 300 FQAEKGLSLALSLWGFVSYFYGEIKSG----EDKRRIQQEESQE 339
                                                                                                                                             6.5%; Score 114.5; DB 4;
19.8%; Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; Mismatches
                                                                                                                                                                                                                                                   Sequence 2922, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 - IMISVLLPITEVLAVI 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 RLLIAAVIVGI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: M.catarrhalis
US-09-540-236-2922
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Best Local Similarity
Matches 51; Conserv
                                                     576 VSG----2
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US-09-489-039A-8024
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US-09-540-236-2922
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                                                             ----WQ-----GFFLGAIGLIFSTSSL 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 IGIVFFFKNIGSTFDQRYSGIPKQLATEIAHKIVVVLLYFSGIMLVLSATIDQAF----T 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 ELAYQKAKQTMSYTLVLEFQLILCLIASIVSVIGMFIAGDFKQA-LPKEAREFKLGEALF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : : : : : : | | | : : | | | 353 BFRWLHSLNPLKFHFILOFPSI---LGFLLIMGRGIAARVKRAXLP---TIFLIULALL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 LYFPVVFLFTTFKKKGFLGGTSLKTQGQLLLVSLLEWTGVLFSFLSVGYLMBIRIDLMQT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 --LLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFWYKHKFTPFT
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Best Local Similarity 19.8%; Pred. No. 0.0021;
Matches 80; Conservative 71; Mismatches 118; Indels 135;
                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 IFIPLLFSYITRRRSNNVGDST-------
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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SEQUENCE DESCRIPTION: SEQ ID NO: 4393:
US-09-107-532A-4393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faccium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: PC
COMPUTER: PC
COMPAGNE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVV-----AVFSAII----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4393:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             SEQUENCES: 7310
                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                             CITY: Waltham
                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                     US-09-107-532A-4393
                                                                                                                                                                                     NUMBER OF
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Patent No. 6562958
GENERAL INFORMATION:
PAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                               294 FTLGLSIFMLIPM--ALVSNYWELGALRFLLGAV----NAAMLPAVQTLILYNITPAIA 346
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        ILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDF----KQALPKEARE 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 ---QHIRHNSELSKIILRLGVPTGIQMITTSMAGL--VIIGLVNHYGSHATAAYGAVNQV 302
                                   FKLGEALFYVVAVFSAII---WQ----GFFLGAIGLIFSTSSLVSGIMISVLLPITEVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 469;
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                                                                                                                                                                        293 -VIFYHEKFQAEKGLSLALSLWGFVSYFYG 321
                                                                                                                                                                                                                                                                                                                  Sequence 5007, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
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Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                    57 YITRRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQ 116
                                                                                                                                                                                                           ---RTRGOS-------PRIVLYMLVGAMQ-----LGIMYLLAFRAYLYLT-- 109
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                                                                                                                                                                                                                                                                                                 -----RKLRWGYLLSAA 145
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                                                                                                                          IVALLIITTILMAFSFSLIGE-----YLAGSVDSYFSVLMRVGLAALVFLPFL-- 73
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  // Score 114; DB 4; Length 325;
// Pred. No. 0.0016;
49; Mismatches 131; Indels 104;
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20.5%; Pred. No. 0.0022;
ive 54; Mismatches 136; Indels 120;
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    6.5%;
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Query Match
Best Local Similarity 22.03
Matches 80; Conservative
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US-09-543-681A-4311
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Sequence 3946, Application US/09134001C

Sequence 3946, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3948
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                                                                             208 QLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVV--AVFSAIIWQGFF---
-GMHTETDKPVHETHKQYITGFLI --TVAAAVMYAFILPLVELAYQKAKQTMSYTLVLEF
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4%; Score 112; DB 4; Length 503;
llarity 23.5%; Pred. No. 0.0047;
Conservative 53; Mismatches 105; Indels 126;
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                                                                                                                                                                                                    275 FGNMGSLFLTGLIFLACMVTAI 296
                                                                                                                                                                  LGAIGLIFSTSSLVSGIMISVL 284
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US-08-898-976-2
; Sequence 2, Application US/08898976
; Patent No. 5891670
; GENERAL INFORMATION:
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Best Local Similarity
Matches 87; Conserv
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US-09-134-001C-3948
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Sequence 7304, Application US/09328352
Sequence 7304, Application US/09328352
Sequence 7304, Application US/09328352
Sequence 7304, Application
Sequence 7304, Application
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DAITE: 199-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 PVSTAALIIASQL--APIAIFSFF-----MVKHKFTPFTINAVVLLTVGAAVL----- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FSTSSLVS------GIMISVLL------PITEVLAVIFYHEKFQAEKGL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 NQOMAKETWIAPILDFFKRYGVKLALVLLFLIGFFRISDIIAGVISNVFYQDLNFSKEQI 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 VISFVLTYIYSGQVTEAISKAGNIQDSAALFGL-EALRFLTATGVALL-VGYLLVKIGVV 308
                                                                                                                                                                                                                                                                                                                                                                                                      140 SAATQDIVIDAYRIELAETEMQTVLASTYNAGYRIGMIVAGAGALFLAAHLGTAKGNYIY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETHKOYITGFLITVAAAVMYAFIL-----PLVELAYQKAKQTMSYTLVLBFQLILCLLA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 SIVSVIGMPIAGDFKQALPK-----EAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLI 269
                                                                                                                                                                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                                                     93 ALGRRR------AMLLIAQCLIVLAICTMAFAD-----PALGHSYLVQMAAGAVLLGF 139
                                                                                                                                                                                                                                                                                                                                                                           114 --ASQLAFIAIFSFFMVKHKFTPF---TINA-----VVLLTVGAAVLGMHTETDKP--VH 161
                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                10 İIALGEMTEALFIGAĞNIIFPPIVAQQAĞDHVWLAAIGFLITAVĞLEVİTİMAL----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 ILAIG------NCGGPLIMRLYFNNGGKRIWFST--FLETA-GFFVIFIPLLFSYITR
                                                                                                                                                                                                                                                                                                  57 YITRRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALII---
                                                                                                                                                                                                                     2 VKALVIINCIILAIGNCGGPLIMRLYFNNGG-----KRIWFSTFLETAGFPVIFIPLLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                           Length 730;
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6.4%; Score 112; DB 4; Length 434;
Best Local Similarity 21.7%; Pred. No. 0.0039;
Matches 70; Conservative 56; Mismatches 112; Indels
                                                                                                                                                                                   Indels
                                                                                                                                           Query Match
6.4%; Score 112.5; DB 4;
Best Local Similarity 21.3%; Pred. No. 0.0069;
Matches 81; Conservative 71; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEAVKVYGVIFSLVGGFLGG 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ', ORGANISM: Acinetobacter baumannii
US-09-328-352-7304
                                                                           TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-09-328-352-7304
                                                                                                              US-09-328-352-4442
                                     SEQ ID NO 4442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 FTFPFIMEQIYHLQLDTTSLLLVPG--YIVAVIVGALSGKIGEYLN----SKQAIITAII 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 ----SFALMYA---PLINEAIKTIDLNMTGVAIGFYNLIINVAVS----VGIAIAAALID 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 IIASQLAFIAIFSFFWVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGF 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 LITVAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAG---D 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 FKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SSHFGIILIILGLMSIV-GLVLFVIL 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%; Score 110.5; DB 2; Length 462; 24.6%; Pred. No. 0.006; tive 43; Mismatches 92; Indels 89
APPLICANT: Lonetto, Michael
APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL TETRACYCLINE RESISTANCE
TITLE OF INVENTION: ROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert
                                                                                                                                                                       ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                     ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 FK----ALNFPGNDAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 462 amino acids
TYPE: amino acid
TYPE: amino acid
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TYPE: amino acid
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Best Local Similarity 24.6*
Matches 73; Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                       USA
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Search completed: September 24, 2004, 00:02:09 Job time: 25.3672 secs

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31-MAY-2002
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(without alignments)
1130.190 Million cell updates/sec
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                                                                                               1 MVKALVIINCIILAIGNCGG......QQEESQETEQSSLSRPISEC 352
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Aag17233
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Aag15104 /
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Aag1467
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Aag44537
Aag15103
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                          1586107 segs, 282547505 residues
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                                                September 23, 2004, 23:33:00
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Maximum Match 100%
Listing first 45 summaries
                                model
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                               protein search, using sw
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geneseqp2004s:*
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Pseudomon	Aau33602	AAU33602	4	296	7.3	129	44
Listeria	Abb47934	ABB47934	ഗ	345	7.6	133.5	43
Protein e	Abu25229	ABU25229	ø	314	7.6	133.5	42
Arabidops	Aag53065	AAG53065	ო	344	7.8	136.5	41
Arabidops	Aag17293	AAG17293	ო	269	7.8	136.5	40
Arabidops	Aag52834	AAG52834	m	336	7.8	137.5	39
Arabidops	Aag23964	AAG23964	ო	336	7.8	137.5	38
Arabidops	Aag23965	AAG23965	ო	333	7.8	137.5	37
Arabidops	Aag52835	AAG52835	ო	333	7.8	137.5	36
Arabidops	Aag23966	AAG23966	ო	277	7.8	137.5	35
Arabidops	Aag52836	AAG52836	ო	277	7.8	137.5	34
Arabidops	Aag17292	AAG17292	m	272	7.8	137.5	33
Arabidops	Aag16233	AAG16233	m	97	7.8	137.5	32
Arabidops	Aag51675	AAG51675	m	286	7.9	139.5	31
Arabidops	Aag32021	AAG32021	ო	323	8.0	140.5	30
Arabidops	Aag53063	AAG53063	m	414	8.0	141.5	29
Arabidops	Aag53064	AAG53064	٣	400	8.0	141.5	28
Arabidops	Aag17291	AAG17291	٣	328	8.0	141.5	27
Arabidops	Aag51674	AAG51674	m	342	8.6	151.5	56

ALIGNMENTS

Herbicidally active polypeptide SEQ ID NO 367. Herbicidal; plant; agriculture; herbicide ABB91156 standard; protein; 351 AA 28-AUG-2001; 2001WO-EP009892. 28-AUG-2001; 2001WO-EP009892. (first entry) Tietjen K, Weidler M; Arabidopsis thaliana. WPI; 2002-269010/31. (FARB) BAYER AG WO200210210-A2.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

Claim 5; SEQ ID NO 367; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

Sequence 351 AA;

99.1%; Score 1744.5; DB 5; Length 351;

61 RRSNNVGDS-----TSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIA

1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR

SQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLIT 174

115

175

235

114

9

Gaps

12;

Length 356; Indels

64.1%; Score 1128; DB 5; 60.1%; Pred. No. 4.5e-112;

66; Mismatches

180

VAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALP 234 KEAREFKLGEALF-YVVAVFSALIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAV 293

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Best Local Similarity 60.1
Matches 215; Conservative
Sequence 356 AA;
                       Query Match
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                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypetides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                  RRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI 120
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                                   1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR
                                                        WYKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLFSYITR
                                                                                                                                                                               YAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREF
              Gaps
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                                                                                                                                                                                                                                                                                       OAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISEC 352
                ;
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                Indels
                ö
   3.3e-178;
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                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidal; plant; agriculture; herbicide
    Pred. No.
                                                                                                                                                                                                                                                                                                                                                            ABB91157 standard; protein; 356 AA
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   99.78;
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                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-269010/31.
   Best Local Similarity
Matches 351; Conserv
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This invention describes a novel nucleic acid encoding a plant nucleobase transporter (I). (I) is produced by complementation of a nucleobase transport (NBT)-defective host cell with a plant gene bank by selection of NBT-positive cells. (I) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the encoded protein (II) in prokaryotic or eukaryotic cells, for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                            for producing transgenic plants with altered encodes a nucleobase transporter protein of
                                                                                                                               PUD1; transgenic plant; nucleobase transporter; apical dominance; flowering behaviour; senescence; pesticide distribution.
                                                                                                                                                                                                                                                                                                                                            Frommer WB;
                                                                                                                                                                                                                                                                                                                                            Andre B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1b; Page 16-17; 24pp; German.
                        AAB10684 standard; protein; 356 AA
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                                                                                                                                                                                                                                                                                       99DE-01007209.
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                             Gillissen B, Buerkle L,
                                                                                                        A. thaliana PUP1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                             nucleobase transport,
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid, useful
                                                                                                                                                                             Arabidopsis thaliana
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N-PSDB; AAA97919.
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990S-0130891P-
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           expression of (II) (when in antisense orientation), and to produce transgenic crop plants. The transgenic plants have modified nucleobase transport properties, e.g. altered effinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in apical dominance, flowering behaviour and sensecence, or improved distribution of pesticides. This sequence represents the Arabidopsis thaliana PUP1 protein which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                    RRSNNVGDS-----TSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIA 114
                                                                                                                                                                                                                                                                                                                                                                                                                           SQLAFIALFSFFWYGHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLIT 174
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                                                                                                                                                                                                                     Ouery Match . 63.9%; Score 1124; DB 3; Length 356;
Best Local Similarity 59.8%; Pred. No. 1.2e-111;
Matches 214; Conservative 66; Mismatches 66; Indels 12; Gaps
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60.0%; Pred. No. 2.1e-49;
ive 32; Mismatches 34; Indels
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               342
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19. P. P. P. P. P. P. P. P. P. P. P. P. P.	Query Match 29.7%; Score 522.5; DB 3; Best Local Similarity 33.8%; Pred. No. 4.5e-47; Matches 116; Conservative 82; Mismatches 126;
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Gaps

68

51 LLLAGETIATLGRLYYEKGGKSTWLETLVOLVGFP-LTLPCYY-YLKPEPSKTKTITKK 108

12 ILAIGNOGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNN---VGD

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                                                                                                                 243
                                                                                                                                   109 TTSSFL---TLSLVYIGLGLLVAGHCILYSFGLLYLPVSTFSLISASQLAFNAVFSYFLN 165
                                                         SQKITPFILNSLVLLTISSTLLVIQHEPESP-SSTSKSAAKSKYVIGYICAVGSSAGYSL 224
                                                                                                                                                                                    EALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAE 303
                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                           184 ILPLVELAYOKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKIG
                                   129 KHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHK-----QYITGFLITVAAAVMYAF
                                                                                                                                                                                                                                                                KGLSLALSLWGFVSYFY----GEIKSGEDKRRIQGEESGETEQ 342
                                                                                                                                                                                                                                                                                     | ::: |:: ||||| | | : | ||| | KLIAMFLAIWGFVSYGYQHYVNDRKPEEDQELPQSKEEEEGKQ 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 67347.
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244 EALFYVVAVESAIIMQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAE 303
                                                                                                                                                                                                                                                                              STSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFMV 128
                                                                                                                                                                      129 KHKETPETINAVVLLIVGAAVLGMHTETDKPVHETHK-----QYITGFLITVAAAVMYAF 183
                                                                                                                                                                                    protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                    184 ILPLVELAYOKAKOTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLG
                                                                                                                                                                                                                                  12 ILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSIN---VGD
                              Length 386;
                            Query Match 29.6%; Score 521.5; DB 3; Length Best Local Similarity 33.8%; Pred. No. 5.66-47; Matches 116; Conservative 82; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                 304 KGLSLALSLWGFVSYFY----GEIKSGEDKRRIQQEESQETEQ 342
                                                                                                                                                                                                                                                                                                                             336 KLVAMPLAIWGFVSYGYQHYVNDRKPEEDQGLPQSKEBEEGKQ 378
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24-SEP-1999; 28-SEP-1999

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21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999;

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159 SQKITPFILNSLVLATISSTLLVIQHEPESP-SSTSKSAAKSKYVIGYICAVGSSAGYSL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                               DB 3; Length 387;
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33.8%; Pred. No. 5.6e-47;
iive 82; Mismatches 126;
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Matches 116; Conservative
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12-OCT-1999
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03-AUG-1999
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STSFFLIXPRILIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFWV 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 KHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHK-----QYITGFLITVAAAVMYAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 EALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                      Length 394;
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                                                                                                                                                                                                                                                                                                                                    29.6%; Score 521.5; DB 3;
llarity 33.8%; Pred. No. 5.7e-47;
Conservative 82; Mismatches 126;
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.3 359 1.15 uS-10-242-525A-201894 Sequence 201894 .3 353 13 uS-10-62-727-79 Sequence 79, p. 3 360 13 uS-10-62-727-136 Sequence 72476 .3 360 13 uS-10-62-727-136 Sequence 72476 .3 362 11 uS-09-864-408A-2569 Sequence 2569, 3 369 13 uS-09-922-293-47449 Sequence 4, Ag. 3 369 15 uS-10-242-535A-47449 Sequence 4, Ag. 3 369 16 uS-10-242-535A-47449 Sequence 474449	1.3 372 13 US-10-424-599-122785 Sequence 12278 1.3 373 13 US-10-424-599-41287 Sequence 41287 1.3 377 9 US-09-770-791-236 Sequence 236, P. 1.3 377 9 US-09-770-791-236	1.3 377 16 US-10-203-72449 Sequence 22449, 1.3 377 16 US-10-242-535-2449 Sequence 22449, 1.3 379 9 US-09-796-692-3163 Sequence 3163, Ap	1.3	1.3 379 16 US-10-154-884B-3163 Sequence 3163, Ap 1.3 379 17 US-10-154-884B-3163 Sequence 3163, Ap 1.3 379 17 US-10-764-324-3163 Sequence 3163, Ap	1.3 382 9 US-09-864-761-31731 Sequence 31731, A 1.3 390 13 US-10-424-599-16750 Sequence 16750,	1.3 391 15 US-10-262-141-10 Sequence 10, Appl	1.3 392 15 US-10-262-3//-10 Sequence 10, Appl 1.3 392 15 US-10-262-141-11 Sequence 11, Appl 1 3 392 15 US-10-262-272-11 Sequence 11, Appl	1.3 393 US-09-768-827-48 Sequence 48, Appl	1.3 397 15 US-10-925-298-10 Sequence 10, Appl 1.3 397 15 US-10-102-806-10 Sequence 10, Appl	1.3 401 9 US-09-795-668-1061 Sequence 1061, 1.3 401 9 US-09-795-686-1061 Sequence 1061,	1.3 401 9 US-09-946-807-1061 Seguence 1061 1.3 407 13 US-10-424-599-50830 Seguence 5083	1.3 408 17 US-10-437-963-29514 Sequence 29514, 1.3 408 17 US-10-437-963-48841 Sequence 48841,	1.3 409 9 US-09-964-824A-52 Sequence 52, P 1.3 415 13 US-10-062-727-992 Sequence 992,	1.3 420 9 US-09-960-352-13951 Sequence 13951 1.3 420 9 US-09-864-761-23834 Sequence 23834 1.3 420 9 US-09-964-761-23834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-20834 1.3 420 9 US-09-964-761-2080 1.3 420 9 US-09-964-761-2080 1.3 420 9 US-09-964-761-2080 1.3 420 9 US-09-964-761-	1.3 428 9 US-U9-88U-1U/-2286 Sequence 2586, 1.3 428 10 US-U9-8144-353-928 Sequence 928, 1.3 428 10 US-U9-814-353-9780	1.3 428 12 US-09-968-0078-267 Sequence 26760 1.3 429 10 US-09-918-995-8760 Sequence 8760	1.3 430 15 US-10-060-036-2483 Sequence 2483 1.3 431 10 US-09-918-995-17484 Sequence 1748	1.3 431 15 US-10-029-386-24658 Sequence 2465 1.3 432 13 US-10-282-122A-19775 Sequence 1977	1.3 432 13 US-i0-282-122A-23354 Sequence 2335 1.3 435 9 US-09-815-242-9842 Sequence 9842,	1.3 435 12 US-09-732-627A-1707 Sequence 1707, 1.3 435 13 US-10-282-122A-39067 Sequence 39067	1.3 437 10 US-09-764-891-6902 Sequence 6902, 1.3 438 13 US-10-027-632-96289 Sequence 96289	1.3 438 13 US-10-027-632-174560 Sequence 17456	1.3 438 16 US-10-027-032-174560 Sequence 17456	1.3 440 12 US-104-52/NA-2395 Sequence 2395, 1.3 441 13 US-10-424-599-74409 Sequence 74409	1.3 441 17 US-10-437-963-91327 Sequence 91327 1.3 443 13 US-10-085-783A-31197 Semience 31197	1.3 443 13 US-10-027-632-43493 Sequence 43493	1.3 443 15 US-10-02/-652-43494 Sequence 43494 1.3 443 16 US-10-027-632-43493 Sequence 43493	1.3 443 16 US-10-027-632-43494 Sequence 43494	1.3 446 10 US-09-918-995-19150 Sequence 19150	1.3 451 13 US-10-276-599-20575 Sequence 20575	1.3 455 17 US-10-767-795-5686 Sequence 5686, 1.3 456 13 US-10-085-783A-55738 Sequence 55738	1.3 456 16 US-10-242-535A-55738 Sequence 55738 1.3 459 13 US-10-0862-783A-36190 Sequence 55738 1.3 459 16 US-10-242-535A-36190 Sequence 36190

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US-10-242-535A-54761
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Sequence 54761, Application US/10085783A

Sequence 54761, Application No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REPERBURC: 4231/2002

CURRENT FILING DATE: 2002-02-28

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-18

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: Patentin version 3.2

LENGTH: 470
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       Sequence 3028, Ap. Sequence 3029, Ap. Sequence 1309, Ap. Sequence 1943, Ap. Sequence 1318, Ap. Sequence 1318, Ap. Sequence 1318, Ap. Sequence 140569, Sequence 140569, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 296421, Sequence 20055, Sequence 370, App. Sequence 370, App. Sequence 370, App. Sequence 20595, Sequence 105095, Sequence 105095, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 129999, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Sequence 105095, Seque
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Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 21; Conservative 0; Mismatches 0; Indels
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Sequence 54761, Application US/10242535A
; Sequence 54761, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2005
; FILE REFERENCE: 4231/2005
; FILE REFERENCE: 4231/2005
; FILE REFERENCE: 2002-02-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-13
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APPLICATION NUMBER: 60/253,625
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100.0%; Pred. No. 6.2;
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in Cancer
FILE REPERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEC ID NOS: 866
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2053, Application US/10087192
| Publication No. US2002018258641
| GENERAL INFORMATION: APPLICANT: MITTE OF INVESTIGNEY OF TITLE OF INVESTIGNEY NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVESTIGNEY NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVESTIGNEY NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVESTIGNEY OF 2002-03-01
| PRIOR FILING DATE: 2002-03-01
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| PRIOR PILING DATE: 2000-12-22
| PRIOR FILING DATE: 2001-03-02
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| NUMBER OF SEQ ID NOS: 2059
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                               FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(end)

S. OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Listeria monocytogenes 4b
                                                                                                                                                                                                                                                                                                                                                                                                                         693 GCTACTTTTTCTGTGTCATT 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 820, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             685 GCTACTTTTTTCGTGTCATT 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(23126)
OTHER INFORMATION: n = A,T,C or G
                                   NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3618
LENGTH: 2791
              PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity 100.0
Matches 21; Conservative
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US-10-087-192-2053
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23082
LENGTH: 1093
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APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REPERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.7%; Score 21; DB 13; Length 729; Best Local Similarity 100.0%; Pred. No. 5.8; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
CTHER INFORMATION: Clone ID: LIB3594-005-F3_FLI
US-10-425-114-23082
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PATENTIN VERSION 3.1
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Publication No. US20040018514A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             ; ORGANISM: Pasteurella multocida
US-10-282-122A-31258
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Best Local Similarity
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US-10-398-221-3618/c
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US-10-425-114-23082
                                                                                                                                                                                                                           SEQ ID NO 31258
LENGTH: 729
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Gaps

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APPLICANT: Xu, H.

JITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITARA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-66
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
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PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PL
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100.0%; Pred. No. 20;
ive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 1000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-03-28
PRIOR FILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 854
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Matches 20, Conserv
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US-10-027-632-121522
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US-10-027-632-121522

Sequence 121522, Application US/10027632

Sequence 121522, Application US/10027632

Sequence 121522, Application No. US20020198371A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REPERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

CURRENT FILING DATE: 2000-0718,006

PRIOR APPLICATION NUMBER: US 60/19,006

PRIOR APPLICATION NUMBER: US 60/19,066

PRIOR APPLICATION NUMBER: US 60/19,066

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE PRACES
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                        DB 17; Length 41787;
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100.0%; Pred. No. 20;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                     1.7%; Score 21; DB 100.0%; Pred. No. 7; tive 0; Mismatches
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; Sequence 121522, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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                             ; LENCTH: 41787
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-820
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Best Local Similarity
Matches 20; Conserv
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; ORGANISM: Human
US-10-027-632-121522
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LENGTH: 854
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US-10-282-122A-24401

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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 73128
SEQ ID NO 9121
LENGTH: 802
TYPP.
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cavolic David K

APPLICANT: Cavolic David K

APPLICANT: Cavo Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION UNDERS: US/10/424,599

CURRENT FILING DATE: 2003-44-28

NUMBER OF SEQ ID NOS: 285684

LEMETHE OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_104214C.1
US-10-424-599-4662
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65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6%; Score 19; DB 100.0%; Pred. No. 65; Live 0; Mismatches
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US-10-425-114-9121
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Pred. No.
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Patent No. US20020144047A1
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Best Local Similarity 100.0%;
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Canou Yihua
APPLICANT: Canou Yihua
APPLICANT: Canou Yihua
APPLICANT: Canou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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OTHER INFORMATION: Clone ID: PAT_MRT3847_138411C.1
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APPLICANT: Budworth, P.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Ann, E.
APPLICANT: Han, B.
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CURRENT FILING DATE: 2001-06-25
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Sequence 13, Application US/08588976
Sequence 13, Application US/08588976
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TITLE OF INVENTION: Methods and Compositions for TITLE OF INVENTION: Inhibiting Hexokinase NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STREET: US
COUNTRY: US
ZIP: 77210
COMPITER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: Detentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/589,976
FILING DATE: CONCURTENTLY herewith CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: 39,458
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REPRENCE/OCKET NUMBER: UTSD:481/FUS
TELEPHONE: (512) 474-7577
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ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARENTIN RC-DOS/MS-DOS
SOFTWARE: PARENTIN RC-DOS/MS-DOS
SOFTWARE: PARENTIN RC-DOS/MS-DOS
APPLICATION NUMBER: US/08/588,983
FILING DATE: CONCURRENTLY herewith
FILING DATE: CONCURRENTLY
ATTORNEY/AGENT INFORMATION:
NAME: FURSEW, Shelley P. M.
REGISTRATION NUMBER: 39,458
REBERENCE/POCKET NUMBER: 1750
TELEFAM: (512) 418-3000
TELEFAM: (512) 414-7577
TELEFAM: (512) 474-7577
TELES: NA
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3647 base pairs
TELENGTH: 3647 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1602 rrdercrcrrcrrcrcaccc 1584
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 3647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 19; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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Sequence 1, Appli
Sequence 11, Appl
Sequence 1, Appli
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Sequence 3, Al
Sequence 38,
Sequence 3, Al
Sequence 3, Al
Sequence 1, Al
                                                                         Sequence 33, Sequence 3, Sequence 3, Sequence 1, Sequence 34, Sequence 34, Sequence 5,
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1.6%; Score 19; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 19; Conservative 0; Mismatches 0; Indels
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US-09-621-976-15356/C

Sequence 15356, Application US/09621976

Patent No. 663963

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 15356

LENGTH: 500
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; Sequence 13, Application US/08588983
; Patent No. 5854067
; GENERAL INFORMATION:
    APPLICANT: Christopher B. Newgard, et al.
    TITLE OF INVENTION: for Inhibiting Hexokinase; TITLE OF INVENTION: for Inhibiting Hexokinase; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: AD
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US-09-873-404-3
US-09-878-853A-3
US-09-245-041-5
US-09-918-512-3
US-09-918-512-3
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US-09-918-512-3
US-09-918-394A-21
US-09-539-333D-1
US-09-579-409-1
US-09-679-409-1
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63588
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810047
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1126592
128779
128779
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CORGANISM: Homo sapiens
US-09-621-976-15356
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US-08-588-983-13/c
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1.5%; Score 18; DB 4; Length 413;
100.0%; Pred. No. 28;
tive 0; Mismatches 0; Indels
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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTE and Encoded Human Proteins.
; PILE REFERENCE: GENSET 1054FR2.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15567
                                                                                         Sequence 15359, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
TITLE OF INTERNITY Glordano, J.Y.
TITLE OF INTERNITY OF SETS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15359
LENGTH: 413
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Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Gendano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-621-976-15359
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Matches 18; Conserv
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US-09-621-976-15367
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                                                                       Score 19; DB 2; Length 3647;
Pred. No. 9.2;
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1.5%; Score 18; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels
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Pred. No. 28;
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Patent No. 6466790
GENERAL INFORMATION: 6466790
JENERAL INFORMATION: METASTATIC BREAST AND COLON CANCER
TITLE OF INVENTION: REQUIATED GENES
TITLE OF INVENTION: REQUIATED GENES
TITLE OF INVENTION: REQUIATED GENES
TITLE OF INVENTION: REQUIATED GENES
TITLE OF INVENTION: REQUIATED GENES
TITLE OF INVENTION NUMBER: US/09/712,016
CURRENT APPLICATION NUMBER: US/09/417,615
PRIOR APPLICATION NUMBER: US/09/417,615
PRIOR FILING DATE: PRIORFILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 85
SEQ ID NOS: 85
SEQ ID NO 15
LENGTH: 304
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US-09-621-976-15361/C
i Sequence 15361, Application US/09621976
j Patent No. 663963
j GENERAL INFORMATION:
j APPLICANT: Dumas Milne Edwards, J.B.
j APPLICANT: Jobert, J.
j APPLICANT: Glordano, J.Y.
j TITLE OF INVENTION: ESTS and Encoded Human Proteins.
j TITLE OF INVENTION: ESTS and Encoded Human Proteins.
j CURRENT APPLICATION WUMBER: US/09/621,976
j CURRENT FILING DATE: 2000-07-21
j NUMBER OF SEQ ID NOS: 19335
j SOFTWARE: Patent.pm
                                                                Query Match 1.6%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 9.2 Matches 19; Conservative 0; Mismatches
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US-09-712-016-15
                                                                                                                                                                 184 TIGGICTCCTTCCTCAGCC 202
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Best Local Similarity 100.
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CORGANISM: Homo sapiens
US-09-621-976-15361
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ORGANISM: Homo sapien
  linear
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; TOPOLOGY:
US-08-588-976-13
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100.0%; Pred. No. 28;
tive 0; Mismatches 0; Indels
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; Sequence 15366, Application US/09621976
; Patent No. 6639063;
GENERAL INFORMATION:
APPLICANT: Domas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSEI.054FR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15366
LENTH: 425
                                                                                                RESULT 11
US-09-621-976-15362/c
; Sequence 15362, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERIC 1054PR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13362
LENGTH: 416
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1S-09-076-15365, Application US/09621976
1 Sequence 15365, Application US/09621976
2 Patent No. 6639063
2 APPLICANT: Dumas Milne Edwards, J.B.
3 APPLICANT: Jobert, S.
3 APPLICANT: Glordano, J.Y.
3 TITLE OF INVENTION: ESTS and Encoded Human Proteins.
3 FILE REFERENCE: GENSET.054PR2
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744 AGAAGCAAGAGAGTTCAA 761
                    354 AGAAGCAAGAGAGTTCAA 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Homo sapiens
US-09-621-976-15362
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Best Local Similarity
Matches 18; Conserv
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US-09-621-976-15366/c
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1.5%; Score 18; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 28;
tive 0; Mismatches 0; Indels
                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 28; Length 414;
Matches 18; Conservative 0; Mismatches 0; Indels
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US-09-621-976-15360/C

Sequence 15360, Application US/09621976

Patent No. 663963

GENERAL INFORMATION:
PAPPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTA and Encoded Human Proteins.
TITLE OF INVENTION: ESTA and Encoded Human Proteins.
CURRENT APPLICANTON NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOGTWARE: Patent.pm

LENGTH: 416
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15358, Application US/09621976; Sequence 15358, Application US/09621976; Patent No. 6639063; GENERAL INFORMATION: APPLICANT: Jobert, S. APPLICANT: Jobert, S. TITLE OF INVENTION: ESTS and Encoded Human Proteins. TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REPERENCE: GENERI-054PR2 CURRENT APPLICATION NUMBER: US/09/621,976; CURRENT FILING DATE: 2000-07-21; NUMBER: OF SEQ ID NOS: 19335; SOFTWARE: Patent.pm; SEQ ID NO 15358; LENGTH: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: 287
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 AGAAGCAAGAGAGTTCAA 761
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                                                                                                                                                                                                                                                              744 AGAAGCAAGAGAGTTCAA 761
                                                                                                                                                                                                                                                                                              354 AGAAGCAAGAGAGTTCAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 18; Conservative
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CRGANISM: Homo sapiens
US-09-621-976-15360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-15364
                             SOFTWARE: Patent.pm
SEQ ID NO 15364
LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-621-976-15358/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Sequence 5, Application US/08741134

| Patent No. 5861498
| GENERAL INFORMATION
| APPLICANT: Litwack, Gerald
| APPLICANT: Litwack, Gerald
| APPLICANT: Litwack, Gerald
| TITLE OF INVENTION: IMMUNOPHILIN FKEP46 AND COMPOSITIONS FOR MAKING
| TITLE OF INVENTION: METHODS OF USING THE SAME
| NUMBER OF SEQUENCES: 6
| NUMBER OF SEQUENCES: 6
| TITLE OF INVENTION: METHODS OF USING THE SAME
| NUMBER OF SEQUENCES: 6
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,134
FILING DATE:
CLASSIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
                                                                                                                                  BARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER PILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Homo sapiens
FRETURE:
NAME/KRY: SITE
LOCATION: (909)
COTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-123
                       APPLICATION NUMBER: 60/055,950
                                                                                                           APPLICATION NUMBER: 60/055,947
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.
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1.5%; Score 18; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels
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Fatenn No. 644281
SERNEAL INFORMATION.
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 15365
LENGTH: 454
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                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15365
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US-09-227-357-123
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FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
ATTORNEY-AGENT INFORMATION:
NAME: Defluca, MarK
REGISTRATION NUMBER: 33.29
REFERENCE/DOCKET NUMBER: 33.29
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REGISTRATION INFORMATION: TELECOMMUNICATION INFORMATION: 215-568-310
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TELECRAK: 215-568-310
TELECRAK: 215-568-310
TELECRAK: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: 1.1.336
USORECULE TYPE: CDN
MARCKEULE TYPE: CDN
MARCKEULE TYPE: CDN
MARCKEULE TYPE: CDS
MACKEULE TYPE: CDS
MACKEULE TYPE: CDS
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Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Sequence 14, Appl

Sequence

US-09-621-976-15639 US-10-204-708-14 US-09-621-976-8976

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Result No.

20, Appl 57, Appl 26, Appl 12, Appl 43, Appl 43, Appl 78, Appl 11, Appl 11, Appl 11, Appl 11, Appl 31, Appl 31, Appl 31, Appl 1, A 3817 Sequence 1 Sequence 4 Sequence 1 Sequence 2 Sequence 4 Sequence 1 Sequence 8 Sequence 3 Sequence 3 Sequence Sequence Sequence Sequence Sequence Sequence 4.0%; Score 48.6; DB 1; Length 7218; COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria US-09-621-976-16140 US-09-621-976-2813 US-09-252-991A-3817 US-09-056-783-1 US-09-107-532A-424 US-09-056-075-1 AFLILMS DATE:
CLASSIFICATION 135
PRIOR PAPELICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
RECISTRATION NUMBER: 29,768
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAN: (703) 895-9300 US-10-204-708-84 US-10-204-708-93 US-09-801-861-3 US-10-204-708-54 US-09-790-988-1 ALIGNMENTS Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION: LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single TELEX: 899149 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 6243 7664 10144 53332 5610 11050 pTZgpt-Fls linear COUNTRY: USA ZIP: 22313-0299 US-08-232-463-14 Query Match

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COUNTIENT (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
OTHER INFORMATION: n is a or g or c or t
FRATURE:
LOCATION: /*^^^
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TILLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
MAME/KEY: unsure
LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (10005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (11703, 11933, 12050, 12340, 12981, 13564, 13764..13765, 13787)
OTHER INFORMATION: n is a or g or c or t
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OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1083 ITATGTTGCTTAATTTCTATAACTCTATACGATTATAACAGAGCATTACTGTTATTT
                                                                                                                                                                                                                                                                                                                                                                            6109)
                                                                                                                                                                                                                                                                              5674)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
OTHER INFORMATION: n is a or g or c or t
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                                                                                                                                                                          LOCATION: (4298, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9879)
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                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, OTHER INFORMATION: n is a or g or c or t
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3.5%; Score 43; DB 4; Length 19233;
Best Local Similarity 56.4%; Pred. No. 0.03;
Matches 79; Conservative 0; Mismatches 61; Indels
                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494,
OTHER INFORMATION: n is a or g or c or t
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CTHER INFORMATION: n is a or g or c or t US-10-204-708-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: unsure
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NAME/KEY: unsure
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US-10-204-708-70
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j Sequence 45, Application US/10204708

j Patent No. 6677731

j GENERAL INFORMATION:

j APPLICANT: OLEK, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: PIEBENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Dy Assessing DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

LEMOTH: 19233

TWOND: DNA
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NAME/KEY: unsure
LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
                                                                                                                                                                                             116 GCGGAAAACGAATCTGGTTCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCTCA
                                                                                                                                                                                                                                                                                              176 TCCCTCTCTTGGTCTCCTTCGTCGCCGTCGCCGCGAACCGCAACCCTAACAACGCGG
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NAME/KEY: unsure
LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
OTHER INPORMATION: n is a or g or c or t
                                                                                                 56 TTATCCTCACTATAGGAACATGTGGAGGTCCTTTGTTAACTCGTCTCTACTTCACCAATG
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                       Best Local Similarity 5.1%; Pred. No. 0.0003;
Matches 21; Conservative 217; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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NAME/KEY: unsure
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US-10-204-708-45
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Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas B.
VENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
YENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
SQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174
                                                                                                              1066 ATTCTTCCAGTTAGTGATTATGTTGCTTAATTTCTATAACTCTATACGATTATAACAGAG 1125
                                                                                                                                                                                                                1126 CATTACTGTTATGTTTGTTCCTAAATATTATGTGTGATTGTGTGTTTTTTGTTATTGTTC 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 Ararrinaggrianagringingingangangangkangkangangang
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                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scallar, Matthew J.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Ali O.
APPLICANT: Gure, Milliamaon, Barbara
APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Cancer Associated Antigens and Uses;
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
TITLE APPLICATION NUMBER: US/09/392,714A
CURRENT APPLICATION NUMBER: US/09.09
EARLIER APPLICATION NUMBER: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 14561
                                                             67; Indels
                                                                                                                                                                                                                                                                    326 GATTATTTTTATTTTTTTTTAAATTATTATTGTGGTAATTTG
                              Best Local Similarity 54.4%; Pred. No. 0.13; Matches 80; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1175 TGTTATTGTTCTTGTGTATAAGTATGAATA 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09392714A Patent No. 6686147
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chitnis, Chet APPLICANT: Miller, Louis APPLICANT: Peterson, Dav APPLICANT: Wellems, Thom APPLICANT: Wellems, Thom TITLE OF INVENTION: BIND TITLE OF INVENTION: AND NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rYPE: DNA
CORGANISM: Homo sapiens
US-09-392-714-1
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Sequence 65, Application US/10204708

Patent No. 677731

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander

APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: PCT/FP01/03971

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

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PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

WHORER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1083 TTATGTTGCTTAATTTCTATAACTCTATACGATTATAACAGAGCATTACTGTTATGTTTT 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1143 GTTCCTAAATATTATGTGTGATTGTGTTTTTTGTTATTGTTCTTGTTGTATAGTATGAA 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.3%; Score 40; DB 4; Length 6040;
Best Local Similarity 57.0%; Pred. No. 0.12;
Matches 73; Conservative 0; Mismatches 55; Indels
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
PRIOR PILING DATE: 2003-05-06
                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-204-708-65
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SEQ ID NO 65

Query Match

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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (234814). (234814)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (309398). (309398)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (309418). (309418)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (98159). (98159)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (98266). (98266)
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (191989)...(191989)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
                                                     LOCATION: (28257)...(28258)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (84773)...(84773)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (84808)...(84808)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature
LOCATION: (84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812)...(84812).
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (312993)...(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
JTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature.
LOCATION: (234220)...(234220)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
   INFORMATION: n equals a,
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LOCATION: (312837)..(312837)
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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US-08-916-421B-1/c

US-08-916-421B-1/c

US-08-916-421B-1/c

US-08-916-421B

EQUIPMENTION:

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ

TITLE OF INVENTION: jannaschii

TITLE OF INVENTION: jannaschii

PALENE REFERRNCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT APPLICATION NUMBER: US 60/024,428

PRIOR PAPLICATION NUMBER: US 60/024,428

PRIOR PELING DATE: 1996-08-22

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 1664976
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Best Local Similarity 56.0%; Pred. No. 0.34;
Matches 75; Conservative 0; Mismatches 59; Indels 0;
                                                                                                                                                                                  ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: ISTEALSEN, NOWER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFIRENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRAX: (619) 235-0356
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
       ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
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NAME/KEY: misc_feature
LOCATION: (28222)..(28222)
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STRANDEDNESS: single
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HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13
                                                                                                                                                         COUNTRY:
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KEY: misc feature
ION: (559241)..(559241)
INFORMATION: n equals a, t,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1130881)..(1130881)
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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TON: (871619)..(871619)
INFORMATION: n equals a,
                                                                                                    NAME/KEY: misc feature
LOCATION: (622708)..(622708).
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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ACATION: (855539)..(855539)
THER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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INFORMATION: n equals a,
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OCATION: (1310988)..(1310988)
THER INFORMATION: n equals a,
                                                                      LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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THER INFORMATION: n equals a, AME/KEY: misc_feature
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COCATION: (1084830)..(1084830)
THER INFORMATION: n equals a,
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INFORMATION: n equals a,
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LOCATION: (741684)...(741684)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (1349473) ..(1349473)
OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
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(779676)..(779676)
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836675 TATCAAAATTTAAACCTGATTTAAAGATTATAGCCGATTTAATTAGAGTTGGAATTCCTT 836616
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APPLICANT: DIEFENBROCK, Christian
APPLICANT: PIEFENBROCK, Thristian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                    590 TTATATTACCGCTCGTTGAGCTAACTTACAAGAAAGCTCGTCAAGAAATCACTTTCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              836855 Trangarageaageerraragecacritraacaaacarcerragaceegararicarer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 TTGTGCTTGAGATTCAGATGGTCATGTGCCTTGCTGCTACTTTTTTCTGTGTCATTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 710 TGTTCATCGTTGGAGATTTTAAGGTGATAGCAAGAGAAGAAGAAGAGAGTTCAAGATTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   770 GATCAGTGTTTTACTATGCATTGATAGTGATCACAGGAATAATATGGCAAGGTTTCTTCT
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                                                                                                                                                                                                                                                                                               Query Match 3.2%; Score 39.4; DB 4; Length 1664976; Best Local Similarity 46.5%; Pred. No. 6.6; Matches 127; Conservative 0; Mismatches 146; Indels 0; G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               836615 caccarrcaracacarracrcrrccacrarcar 836583
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PRIOR PELING DATE: 2001-04-06

PRIOR PELING DATE: 2001-04-06

PRIOR PELING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PELING DATE: 2000-04-07

PRIOR PELING DATE: 2000-04-07

PRIOR PELING DATE: 2000-04-07

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

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Patent No. 6677731
CTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
CTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (1664854)..(1664855);
US-08-916-421B-1
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GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BERNES, DEBRA D.
APPLICANT: BERNES, DEBRA D.
APPLICANT: MELSON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: UNMER: US/09/580,995A
CURRENT PILING DATE: 109-6
FRIOR APPLICATION NUMBER: US/09/80,361
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-09-14
PRIOR FILING DATE: 1996-09-14
PRIOR FILING DATE: 1996-09-14
PRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATCHTIN UNFER: US/10,51
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                                       708 CATGITCALCGITGGAGAITITIAAGGTGATAGCAAGAGAAGCAAGAGAGITCAAGAITGG 767
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828 CITAGGAGCCATAGGGATTGTGTTTTTGTGCATCACCACCTAGCTTCTGGTGTTCTGATAAG 887
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Pred. No. 0.31;
0; Mismatches 149; Indels
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                                                                                    888 IGTICTGCTTCCGGTGACTGAAGTTTTCGCCGTCGTT 924
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Patent No. 6143559
GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
                                                                                                                                                                                                                             Sequence 2, Application US/09588995A
Patent No. 6514697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Cryptosporidium parvum US-09-588-995A-2
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Best Local Similarity 46.2%;
Matches 128; Conservative
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          6054 radicitratesfrakosfasirtidartritritritritatekartsfaaridistrita 6113
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COMPUTER: IBM PC compactible
CORPUTER: IBM PC compactible
CORFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
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Pred. No. 0.31;
0; Mismatches 149;
                                                          1136 ATGTTTTGTTCCTAAATATTATGTGTGATTGTGTGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: PETERS, VERNY, JONES & BIKSA
: 385 Sherman Avenue, Suite 6
Palo Alto
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PILING DATE: 13.5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VERTY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08928361B; Patent No. 6071518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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3.2%;
Best Local Similarity 46.2%;
Matches 128; Conservative
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5511 base pairs
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-08-928-361B-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PETELS (CAROLY)

TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS

TITLE OF INVENTION: SPECIES INFECTIONS

TITLE OF INVENTION: SPECIES INFECTIONS

TOMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSES: PETERS, VERNY, JONES & BIKSA

STREET: 385 Sherman Avenue, Suite 6

CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1134 TTATGTTTTGTTCCTAAATATTATGTGTGATTGTGTGTTTTTTGTTATTGTTCTTGTGTAT 1193
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CURRENT APPLICATION DATE:
BLING DATE: 12-SEP-1997
          SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38.6; Di
Pred. No. 0.31,
0; Mismatches
                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEFHONE: 512/418-3000
TELEFRAX: 512/418-3000
TELEFRAX: 512/418-3000
TELEFRAX: 512/414-7577
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/026,062
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAMME: Verry, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-928-361B-1/c
; Sequence 1, Application US/08928361B
; Patent No. 6071518
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Best Local Similarity 55.6%;
Matches 74; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                              CURRENT APPLICATION DA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-907-146-21
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Sequence 21, Application US/08907146

Patent No. 6316600

GENERAL INFORMATION:
APPLICANT: Michael, Nancy M
APPLICANT: Accavitti, Marianne
APPLICANT: Thompson, Craig B
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
       METHODS FOR THE PRODUCTION OF CHICKEN MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                      ZIP: 77210
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,359
FILING DATE: CONCURRENT! Herewith
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L
REGISTRATION NUMBER: 37,642
REGISTRATION NUMBER: 37,642
REGISTRATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFRAN: 512/418-3000
TELEFRAN: 512/418-3000
TELEFRAN: 512/418-3000
TELEFRAN: 512/418-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
TENTHY: 5526 base pairs
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TITLE OF INVENTION: METHODS FOR THE TITLE OF INVENTION: MONOCLONAL ANTII NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                      STREET: P.O. BCCITY: Houston STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-907-146-21
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Best Local Similarity 58.1%;
Matches 86; Conservative
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US-10-204-708-61
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: BETERSEN, RICHAR A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: 180/19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-00-12
PRIOR FILING DATE: 1997-00-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
SOUTHARE: PARENTING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOUTHARE: PARENTING DATE: 1995-04-03
LENGTHARE: DATE: 1995-04-03
LENGTHARE: DATE: 1995-04-13
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3.2%; Score 38.6; DB 4; Length 7334;
Best Local Similarity 46.2%; Pred. No. 0.38;
Matches 128; Conservative 0; Mismatches 149; Indels 0
                                                                                                                                                                                                                                                                             Query Match 3.2%; Score 38.6; DB 3; Length 7334; Best Local Similarity 46.2%; Pred. No. 0.38; Matches 128; Conservative 0; Mismatches 149; Indels 0
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      480.76-1 (HV)
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; Patent No. 6514697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Cryptosporidium parvum
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEPK: 650-324-1678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERICTICS:
LENGTH: 7334 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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US-08-928-361B-1
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US-10-204-708-04

j Sequence 61, Application US/10204708

j Requence 61, Application US/10204708

j Patent No. 6677731

j GENERAL INFORMATION:

j APPLICANT: DIEKE, Alexander

j APPLICANT: DIEKE, Alexander

APPLICANT: DISTRIBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: DJ ASSESSING DNA Methylation

j TITLE OF INVENTION: DJ ASSESSING DNA Methylation

j TITLE OF INVENTION: UNMBER: VS/10/204,708

CURRENT APPLICATION NUMBER: PCT/EP01/03971

PRIOR FILING DATE: 2000-04-06

pRIOR FILING DATE: 2000-04-06

pRIOR FILING DATE: 2000-04-06

pRIOR FILING DATE: 2000-04-06

pRIOR FILING DATE: 2000-04-06

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-04-07

pRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

seQ ID NO 61

provent. 60-1
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648 ACTIGICCTICAGAITCAGAIGGICAIGTGCCTIGCTGCTACTITITICTGTGTCAITGG 707
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                                                   CATGTTCATCGTTGGAGATTTTAAGGTGATAGCAAGAGAAGCAAGAGAGTTCAAGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.4; DB 4; Length 6801;
Pred. No. 0.41;
0; Mismatches 61; Indels 1.
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September 25, 2004, 09:57:41; Search time 649 Seconds . (without alignments) 9560.189 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                               1 aaaaacagcaagcaagcaagaa.......aatttgaaagatattgagct 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3337386 seqs, 2532474682 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1225
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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		73501,	30274,	10516,	57539,	82061,	102519,	97043,	212, Ap	2212, A	13687,		31364,	9, Appl	91425, A	
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 2212, Ap	Sequence 2212, Ap	Sequence	Sequence	Sequence	Sequence	Sequence	
	ΙD	US-10-424-599-73501	US-10-424-599-30274	US-10-425-114-10516	US-10-437-963-57539	7 US-10-437-963-82061	US-10-424-599-102519	US-10-424-599-97043	US-09-938-842A-2212	US-09-938-842A-2212	US-10-425-114-13687	US-10-437-963-72452	US-10-424-599-31364	US-10-416-898-9	US-10-437-963-91425	
		13	13	13	11	11	13	13	0	11	13	11	13	17	11	
	Query Match Length DB	994	1233	1146	1173	1513	2214	1417	3387	3387	1296	789	1373	83698	1177	
ф	Query	26.6	24.2	24.1	17.4	11.4	11.2	10.5	10.4	10.4	10.3	10.0	9.6	9.6	9.5	
	Score	326	296.4	295.8	212.6	139.2	137.8	128.4	127.2	127.2	126.6	122.4	117.4	117.2	112.8	
	Result No.	-	7	e	4	ບ	9	7	8	o,	10	11	12	13	14	

	Seguence 43860, A	Segmence 61310. A		2524		75161.		1885		Sequence 28473. A							Sequence 6806, Ap	Sequence 9213, Ap			404			Sequence 123, App			~	N	a	_	Sequence 3302, Ap
	US-10	l3 US-10-424-599-61310	US-10-425-	US-1	114-	US-10		US-10	.3 US-10-425-114-12485	13 US-10-425-114-28473	US-10	US-10	9	.7 US-10-437-963-83900	US-10	17 US-10-767-701-9000	17 US-10-767-701-6806	13 US-10-424-599-9213	us-	13 US-09-770-152-44	.7 US-10-767-701-4045	us-	.7 US-10-767-701-4026	.7 US-10-433-793-123	13 US-10-424-599-74177	US-10-311	15 US-10-311-455-78	17 US-10-257-166-2	15 US-10-312-841-2	15 US-10-312-841-1	9 US-09-938-842A-3302
	2381 1				1333			•	•	1779 1	•	2928 1		2605 1	1432 1		747 1	•		592 1				83391 1	486 1	14006 1			3673778	3673778	2000
	0.6	6.8	8.6	9.8	8.5	8.3	7.4	7.2	7.0	7.0	7.0	6.9	6.8	6.7	6.1	5.8	5.5	5.0	4.8	4.5	4.5	4.4	4.1	4.0	4.0	3.9	9.8	3.9	3.9	3.8	3.7
	110.2	108.6	105.8	105	104	101.2	90.4	87.8	98	98	85.4	83.4	83	82	74.2	71	67.4	61.2	58.8	22	52	54.4	50.6	49	48.4	48	47.2	47.2	47.2	46.2	45.6
•	c 15	16	17	18	13	20	21	c 55	23	24	25	56	c 27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	c 45

ALIGNMENTS

ULT 1 10-424-599-73501 10-424-599-73501 40-424-599-73501	Score 326; DB 13; Length 994; Pred. No. 7.4e-84; ; Mismatches 330; Indels 16; Gaps 3;	aaacagcaagcaagaagaagaagaagaagagaattagataga	TCACTATAGGAACATGTGGAGGTCCTTTGTTAACTCGTCTTGTTCACCAATGGCGGAA 121	122 AACGAATCTGGTTCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCTCTC 181
RESULT 1 US-10-424-599-73501 US-10-424-599-73501 Sequence 73504, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION: APPLICANT: La Rosa Thomas J APPLICANT: Cao Vanic David K APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223) B CURRENT APPLICANT: 003-24-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 73501 LENGTH: 994 TYPE: DNA ORGANISM: Glycine max PERATURE: PERATURE: COTHER INFORMATION: Clone ID: PAT_MRT3847_37387C.1	Query Match 26.6%; Score 326; D Best Local Similarity 62.2%; Pred. No. 7.4 Matches 570; Conservative 0; Mismatches	Oy 2 AAACAGCAAGCAGCAAGAAGAAGAAGAAGAAGAAGAAGAA	Oy 62 TCACTATAGGAACATGGAGGTC Db · 155 TCACCATCGGCACCTCCGGTGGGG	Oy 122 AACGAATCTGGTTCATGAGCTTCC

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375 255 255 435 315 495

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GCATCATCACTAGCTTCTGGTGTTCTGATAAGTGTTCTGCTTCCGGTGACTGTTTC
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                                                                                           Length 1233;
                                                                                                                              Indels
                                                                                         Query Match
24.2%; Score 296.4; DB 13;
Best Local Similarity 62.4%; Pred. No. 3.6e-75;
Matches 481; Conservative 0; Mismatches 287;
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12733C.1
US-10-424-599-30274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10516, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
; APPLICANT: Screen, Steven E
; APPLICANT: Caoo, Yongwei
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US-10-425-114-10516
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; Sequence 30274, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Caco Yongwei
; TITLE OF INVENTION: SOy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 12030-04-28
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 30274
; TYPE: DNA
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                                                  TCTTGGTCTCCTTCCTCAGCCGTCGCCGCACCGCAACCTAACAACGAAAACA
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TAACGGAAGTGTTGGC 994
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US-10-424-599-30274
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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Pred. No. 9.5e-51;
0; Mismatches 469;
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US-10-437-963-57539
               Sequence 57539, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                      Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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Best Local Similarity 52.7%;
Matches 542; Conservative
                                                                                                   유.
                                                                                             APPLICANT: La Roga, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Oryza sativa
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERENCE: 38-21 (53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 UNUMBER OF SEQ ID NOS: 73128 SEQ ID NO 10516 LENGTH: 1146
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Sequence 102519, Application US/10424599
; Sequence 102519, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: APPLICANT: Cao Vongwei
    TITLE OF INVENTION: Sy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REPERBNCE: 38-21(5322)B
    CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT PLING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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                                                                                                               533 AGAAAGAGTATGTGGTTGTTGATGACTGTGGTTGCAGCTCTTCTCTATGCTTTTA
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11.2%; Score 137.8; DB 13; Length
Best Local Similarity 50.6%; Pred. No. 9.3e-29;
Matches 359; Conservative 0; Mismatches 347; Indels
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US-10-424-599-102519
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LENGTH: 2214
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Youngei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 82061
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11.4%; Score 139.2; DB 17; Length 1513;
Best Local Similarity 50.5%; Pred. No. 2.8e-29;
Matches 391; Conservative 0; Mismatches 378; Indels 5;
                         CITGAGATICAGATGGTCATGTGCCTTGCTGCTACTTTTT
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US-10-437-963-82061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 82061, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
PILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 987 AGCTATGTTTCATGGGAACTGCAGGAATGCTATTCCTGACATCTTCATTGACTGGGGGGA 1046
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                                                                                     517 GGGGAAACTCCTACCTTCCGTTTTCAACCTCAGCACTTTTGCTATCTTCCCAACTACTCT
                                                                                                                                             TCAACGCTCTTCGCTTTCTTGTTAGTCAAGCAAAAGTTCACTCCGTTCTCCATAAACG
                                                                                                                                                                                            577 TCAACCTTCTCTCTCTCTCATCATGAAGCAAAAAATAACCTTTCCAAACGTGAACT
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PRIOR FILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 3387
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49.6%; Pred. No. 3.8e-26;
tive 0; Mismatches 361; Indels
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                                       Length 3387;
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                                      Score 127.2; DB 9;
Pred. No. 1.5e-25;
0; Mismatches 418;
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2212
                                         Query Match 10.4%;
Best Local Similarity 48.2%;
Matches 391; Conservative
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Sequence 2212, Application US/09938842A publication No. US20040009476A9 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel APPLICANT: Wang, Xun

RESULT 9 US-09-938-842A-2212

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PLANTS, TRANSGENIC PLANTS CONTAINING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 ACCATICITGGATCAGTTIACAICGITACTGGACIATIAGTGTCTGCIAACTCTTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 TATTCTTACGGATTAGCATATCTGCCAGTTTCAACTTCATCGCTCATAATCGGAACTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 CTAGCTITICAACGCTCTCTTTCTTTGTTAGTCAAGCAAAAGTTCACTCCGTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 3387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.2%; Pred. No. 1.5e-25;
Matches 391; Conservative 0; Mismatches 418;
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STREESS-REGULATED GENES OF PLATITIE OF INVENTION: SAME, AND METHODS OF USE
FILE OF INVENTION: SAME, AND METHODS OF USE
CURENT PLANCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT PLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; TYPE: DNA; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2212
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Sequence 72452, Application US/10437963
; Sequence 72452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INPORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cabu, Yihua
; APPLICANT: Chou, Yihua
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brad
; APPLICANT: Brad
; APPLICANT: Brad
; APPLICANT: Brad
; APPLICANT: Ali, Ping
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5321)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 72452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286
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      -----TCGTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTC
                                                                                                                                                           644 CCTACAAGTGCGCCGCGGGGGGGGGACGCCCCGTGACGTACGCGCTAGTGGTGGAGTTGC
                                                                                                                                                                                                                    704 AGCTGGTGATGGGGTTCGTCGCCACCGCTTCTGCACCGCTCGCATGATCGTCAACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TAAACTGTATTATCCTCACTATAGGAACATGTGGAGGTCCTTTGTTAACTCGTCTTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 TCAACTGCGGGATGCTGGTGGTGGGCACCACGGGCCGGGCCGATCCTTAGCCGGCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_72830C.1
                                                                                                                                                                                                                                                                                                                                             725 ATTTTAAGGTGAT 737
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                                                                                                     614 CTTACAAGAAAGC-
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-437-963-72452
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screals, David K.
APPLICANT: Screan, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
1093 TCATTTGTCTATCAGCACTACCTCGACGAAAGAAGTTGAAGACTAGCCACACAAGTCCT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 dchacandacandececececereriagiaecancendracerenagiacircacarinades 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 CATGIGGAGGICCTITGITAACTCGICTCTACTICACCAATGGGGAAAACGAATCTGGT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 TCACCGGTGGGCAGCTCCTCAGCGCCTCTACTTTAGCAAGGGCGGACACCGGCAGTGGC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCATCGCTCTCTTTGGTCTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCAGCCGTCGCCGCGCAACCGCAACCCTAACAACGGGGAAAACAAGCGGAAAACAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTCTTCCTCATGGAAACTCCTCTGTGGAGCGCCTCCATTGTCATAGGGTTGCTCACAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTTGACAACTACTTATATTCTTACGGATTAGCATATCTGCCAGTTTCAACTTCATCGC 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1153 GTAGGAGATCCTCATCTACTACTGCTGAGGA 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-024-D8_FLI
US-10-425-114-13687
                                                            1051 GAGACAGAACTGCCTATTCTTCCAGTTAGTGA
                                                                                                                                                                                                                                                                    Sequence 13687, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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ORGANISM: Zea mays
                                                                                                                                                                                                           RESULT 10
US-10-425-114-13687
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LENGTH: 1296
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                       TGGAGATTTTAAGGTGATAGCAAGAGAAGCAAGAGTTCAAGATTGGAGGATCAGTGTT
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Publication No. US20040172670A1

GENERAL INFORMATION:

APPLICANT: Walker, Elsbeth

APPLICANT: Walker, Elsbeth

APPLICANT: Dellaporta, Stephen

ITLE OF INVENTION: NUMBER: US/10/416,898

CURRENT FILING DATE: 2003-05-16

PRIOR APPLICATION NUMBER: US/10/416,898

CURRENT FILING DATE: 2001-11-16

PRIOR PILING DATE: 2001-11-16

PRIOR FILING DATE: 2000-11-16

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.1
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Pred. No. 1.1e-21;
0; Mismatches 388; Indels
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Best Local Similarity 48.1%;
Matches 363; Conservative (
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CORGANISM: Zea mays
US-10-416-898-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 83698
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US-10-424-599-31364
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
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APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT PPLICATION WNDER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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Publication No. US20040123343A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 91425
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_90000C.1
US-10-437-963-91425
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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US-10-437-963-91425
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                                                                                 3; Gaps
                                             Query Match 9.0%; Score 110.2; DB 17; Length 2381; Best Local Similarity 47.8%; Pred. No. 1.1e-20; Matches 353; Conservative 0; Mismatches 383; Indels 3;
, OTHER INFORMATION: Clone ID: PAT_MRT4530_46977C.1
US-10-437-963-43860
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S Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama, K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Muramatun,M., Hayashizaki,Y. and Shinozaki,K.

Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-960
Email: meeki@rtc.riken.go.jp
               BG439880 GA E8000
CK243751 BST72738
CK251846 BST731555
CK25189 EST7311555
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.rlken.go.jp/e/plant/index_e.html) for further details.
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/clone lib="RAFLI7-32-017"
/note="Site l: BamH1; Site 2: Sall; Subtraction Library.
The sequence was obtained from samples subjected to dehydration-treated (1, 2, 5, 10 and 24 hr) and rehydration-treated (1, 2, 5, 10, and 24 hr) and dehydration treatment)"
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                                                                                                                                                                                                                1. .645
/organism="Arabidopsis thaliana"
/mol_type="mkNA"
/db_xref="taxon:3702"
                                                                                                                                                                                     Location/Qualifiers
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Matches 610, Conservative
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RESULT 2 BH601144

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BH601144 784 bp DNA linear GSS 15-DEC-2001
BOHJF33TF BOHJ Brassica oleracea genomic clone BOHJF33, genomic
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                                                                                                                                                           Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 784)
Town, C.D., Van Aken, S., Utterback, T., Koo, H., and Fraser, C.M.
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/done="BOHJF33"
/clone="BOHJF33"
/clone="BOHJF33"
/clone="BOHJ**
/mole="Wetcor: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
                                                                                                                                                                                                                          Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other GSSs: BOHJF33TR Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11,
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Pred. No. 9.6e-80;
0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cdcown@tigr.org
DNA is from a doubled haploid provided by
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
                                                                                     BH601144.1 GI:17853590 GSS.
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llarity 79.8%;
Conservative (
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                                                                                                                                         Brassica oleracea
                                                      survey sequence.
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199 CTTCACGCGGACGGTGACAAGCTCCCCAAGGAGACGCGCAAGGAGTATATAGTTGGGTTT 140
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Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 688
/ Organism="Brassica oleracea"
/ Ani type="genomic DNA"
/ strain="TOMOODH3"
/ Ab xref="Rocan: 3712"
/ Clone="BOGES"
/ Clone=libe=BOGES"
/ Clone=libe=BOGES"
/ Clone=libe=BOGE"
/ Clone=libe=BOGE"
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/ Clone=libe=BOGES"
/ Clone=libe=BOGES"
/ Clone=livector: pHOS1; Site_I: BstXI; 2-3 kb sheared
/ Clone=livector: pHOS1; Site_I: BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.3%; Pred. No. 1.9e-68;
Matches 482; Conservative 0; Mismatches 179; Indels 15;
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BOGES04TR BOGE Brassica oleracea genomic clone BOGES04, genomic
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Brassica oleracea
Brataryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 688)
1 (pan, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Cother GSSs: BOGES04TF
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                                                                                                                   /mol_type="mkNA" |
/db_xref="taxon:3702" |
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/clone lib="RAFL17" |
/note="Site_1: BamHI; Site_2: SalI; Subtraction Library.
The sequence was obtained from samples subjected to dehydration-treated (1, 2, 5, 10 and 24 hr) and rehydration treatment) |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1025 AAGTIGITGATAAACCICAACCGCCGGAGACAGAA-CIGCCTAITCTICCAGTIAGIGAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 378.8; DB 9; Length 98.4%; Pred. No. 4.6e-75; tive 0; Mismatches 2; Indels
                                                                                                      'organism="Arabidopsis thaliana"
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                                                         cocation/Qualifiers
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Matches 435; Conservative
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Gossypium arboreum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II, Majvales; Malvaceae; Malvoideae; Gossypium.

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Contact: Wing RA

Clemson University Genomics Institute

Clemson University Genomics Institute

Clemson University

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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                      GA Ea0005C03f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA Ea0005C03f, mRNA sequence.
BG439880. GI:13349537
                    409
                                                       382
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
                    CCAGTTTCAACTTCATCGCTCATAATC-GGAACTCAACTAGCTTT----CAACGCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 ACTACTTATATTCTTACGGATTAGCATATCTGCCAGTTTCAACTTCATCGCTCATAATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
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/mol_type="mRNA"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 621.
Location/Qualifiers
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/clone="GA_Ea0005C03f"
                                                                                                                                          410 TCGCTTTCTTGTTAGTCAAGAAA 434
                                                                                                                                                                                                        360 cGGNTTTCTTGTTAGTCAAGCAAAA 384
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//clone_lib="lambda-PRL2"
//clone_lib="Vector: lambda Zip-Lox; Site_l: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
same plants as 3 but aerial tissue (stems, flowers and
sliques. The vector is BRL's lambda Zip-Lox. The cDNA
librars were directionally cloned with Sal-Not arms using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GTCATAGGGTTGCTCACAGGACTTGACAACTACTATATTCTTAGGG-TTAGCATATCTG 299
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MSU-DOB-PRL, Michigan State University, Plant Biology Bldg., E.
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26.4%; Score 322.8; DB 14; Length 589;
Best Local Similarity 95.1%; Pred. No. 2.2e-62;
Matches 366; Conservative 0; Mismatches 13; Indels 6;
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/mol type="mRNA"
/strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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MSU-DOE Plant Research Laboratory
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Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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Enation of ESTS from potato callus tissue

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tig.corg

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                            CK243751

SST7273388 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCA540 5' end, mRNA sequence.
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                                                                                                            CAGGAATAATATGGCAAGGTTTCTTTAGGAGCCATAGGGATTGTGTTTTGTGCATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMVSport6.1; Site 1: EcoRI; Site_2: supplier: RNA was isolated from Solanum tuberosum va Kennebec callus tissue grown on solid media."
      CTGTGGTTGCAGCTCTTCTCTTTTATATTACCGCTCGTTGAGCTAACTTACAAGA
                                                 AAGCTCGTCAAGAAATCACTTTCCCCACTTGTGCTTTCAGATGGTCATGTGCCTTTG
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/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCA540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="callus"
/lab_host="DH10B-TonA"
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Solanum tuberosum
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                                      18 GAAGAAGAAGAATGGTTTGATAATCATAAACTGTATTATCCTCACTATAGGAACATG
                                                                                                                                                          CAGCCGTCGCCGCGCAACCCCTAACAACGCGGAAAACAAGCGGAAAAGCT
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              28; Gaps
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0; Mismatches 393; Indels
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CK251896 1013 bp mRNA linear EST 12-DEC-2003 EST735533 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCER03 5' end, mRNA sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamilds; Solanales; Solanaceae; Solanum.

1 (bases 1 to 1013)

Buell, C.R., Hatt, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from potato callus tissue
                                                   557
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/lab host="DH10B-TonA"
/clone_lib="potato callus cDNA library, normalized and
/ull-length"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 CATTTCTGCTACTGTTTTTTGCACTATTGGAATGGTTATCAACAAGGATTTCCAGGCGAT
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                                                                                                          489 CCGGGCGAACGGTGACCGGCCGGCGAGGTCCACGAAGGATTATATGTTGGGGTTTGT
                                                                                                                                                                            GATGACTGTGCTTGCTCTTCTCTATGCTTTTATATTACCGCTCGTTGAGCTAACTTA
                                                                                                                                                                                                                                      549 GAIGACGTITAICGGTGCGGTGTIAIAIGGAITGAIGTGCCGTIAATTGAGTTGATTTA
                                                                                                                                                                                                                                                                                                        618 CAAGAAAGCTCGTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCAGATGGTCATGTG
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seg primer: ATT TAG GTG ACA CTA TAG.
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/clone="POCBR03"
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/cultivar="Kennebec"
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985 bp mRNA linear EST 12-DEC-2003
EST741103 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POCD557 5' end, mRNA sequence.
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Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue
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full-length"
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Pred. No. 1.1e-55;
0; Mismatches 383; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-array@tigr.org.compara.ne.medical centested from TIGR via potato@tigr.org Seq primer: ATT TAG GTG ACA CTA TAG.
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/organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4113"
/clone="POCD557"
/tissue_type="callus"
/lab_host="DH10B-TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Kennebec"
                                                                                                                                                                                                                               Solanum tuberosum (potato)
                                                                                                                                                              CK257466.1 GI:39814446
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Best Local Similarity 58.2
Matches 570; Conservative
                                                                                                                                                                                                                                                                  Solanum tuberosum
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Solanum tuberosum (potato)

Solanum tuberosum (potato)

Solanum tuberosum (potato)

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Suberryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Suberryota; Viridiplantae; Streptophyta; Euchiote;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; Solanaceae; Solanum.

NCE 1 (bases 1 to 998)

CRS Generation of ESTS from potato callus tissue

NT Contact: Robin Buell

The Institute for Genomic Research

The Institute for Genomic Research

Syll Medical Center Dr. Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

Location/Qualifiers
                                                                                                         CK247918 5998 bp mRNA linear EST 12-DEC-2003 EST731555 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCAX15 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: No
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGAAGATGATTTGATAATCATAAACTGTATTATCCTCACTATAGGAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 288; DB 14; Length 998;
Pred. No. 1.7e-54;
0; Mismatches 380; Indels 2
/organism="Solanum tuberosum"
/mol type="mRNP"
/cultiva="Kennebec"
/db_xref="taxon:4113"
/clone="POCAX15"
/tissue_type="callus"
/lab_host="DH10B-TonA"
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ilarity 58.0%;
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Matches 563;
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                                                                                                                                    DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
KEYWORDS
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                                                                                    RESULT 11
CK247918
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                                                                                                                                                                                                                                  TGGAGGTCCTTTGTTAACTCGTCTTTCACCAATGGCGGAAAACGAATCTGGTTCAT 137
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                                                                                                                                                                                     CAGCCGTCGCCGCGGAACCGCAACCTAACAACGCGGAAAACAAGCGGAAAACAAAGCT
               Var
         supplier: RNA was isolated from Solanum tuberosum Kennebec callus tissue grown on solid media."
                                                                                                                         28;
                                                                                     DB 14; Length 1013;
                                                                                       Score 289.6; DB 14; Length
Pred. No. 7.4e-55;
0; Mismatches 389; Indels
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                                                                                       23.6%;
58.2%;
                                                                                                                           Conservative
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Matches 581;
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124 GGAAATTCAAGGACCCG-----
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al Similarity 58.2%;
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CAACGCGACTCAACTTGCGTTCACTGCGCTTTTTGCTGGTTATAGTTAAACAGAAATT 420
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1 (Dases 1 to 907)

Buell, C.R., Hatt, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue
Umpublished (2003)
                                             497
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                                            CACTCCGTTCTCCATAAACGCCGTCGTTTTGTTGACGGTTGGTATCGGGATCCTTGCGTT
                                                                    421 GACAGCGTATTCGACGAATTCCGTCGTTTTGCTTATCGCCGGAGCTGCGACTTTAGCTCT
                                                                                                ACACAGTGATGGAGACAAACCGGCTAAGGAGAGAAAAAAGAGTATGTGGTTGGGTTCTT
                                                                                                                                                       GATGACTGTGCTTGCAGCTCTTCTCTATGCTTTTATATTACCGCTCGTTGAGCTAACTTA
                                                                                                                                                                                 GATGACGTTTATCGGTGTGTTATATGGATTGATGTTGCCGTTAATTGAGTTGATTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seg primer: ATT TAG GTG ACA CTA TAG.
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9712 Medical Center Dr, Rockville, MD 20850,
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/cultivar="Kennebec"
/db_xref="taxon:4113"
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/tissue type="callus"
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/lab_host="DH10B-TonA"
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full-lend lib="potato callus cDNA library, normalized and
full-lend lib="potato callus callus callus tissue grown on solid media."
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Pred. No. 4.2e-52;
0; Mismatches 361; Indels
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BST735642 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCER86 5' end, mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
I (bases 1 to 979)
Buell, C.R., Hatt, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
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                         498 ACACAGTGATGGAGACAAACCGGCTAAGGAGAGGAGAAAAAAAGAGTTGGGTTGGGTTCTT
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                                                                                  438 CACTCCGTTCTCCATAAACGCCGTCGTTTTGTTGACGGTTGGTATCGGGATCCTTGCGTT
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Other ESTs: EST735643
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: pocato-array@tigr.org
Clones can be requested from TIGR via potato@tigr
Seq primer: ATT TAG GTG ACA CTA TAG.
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1. (bases 1 to 988)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="Deline" /lab host="Deline" /lab host="Deline" | callus con library, normalized and /clone_lib="potato callus con library, normalized and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 GAAAATGAAGAAGCTTATCTTCCTAATTTTCAACATAATTATGCTTTCAATCGCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 TGGAGGICCITIGITAACICGICTCTACTICACCAAIGGCGGAAAACGAAICTGGITCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 GAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCATCCTCTTTTTTGGTCTCCTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 CAGCGTATTACAAACTGTTGTTGTTGTTATTCTCATCCTCTAGCCATAGCCTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCGTCGCCGCGGCAACCGCAACCCTAACAACGGGGAAAACAAGCGGAAAACAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 cgrcritatcacacegeaagagrrcarcecarcrecegegercegaarcarceregerer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 GAAGAAGATGAAGAATGGTTTGATAATCATAAACTGTATTATCCTCACTATAGGAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 CCAACGCCGGAAAATTCAAGG--------ACCCGAGGCTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.5%; Score 275.6; DB 14; Length 988; Best Local Similarity 57.8%; Pred. No. 1.1e-51; Matches 565; Conservative 0; Mismatches 384; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Solanum tuberosum"
                                  TIGICICITACTICIACGCCGAGITIAAA 1014
                                                                         rrgiricararitriargergaarargaa 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCAZ44"
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                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (potato)
                                                                                                                                                                                                                                                                          CK248243.1 GI:39798187
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                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum
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AUTHORS
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                                                                                                                                                RESULT 13
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LOCUS
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BST728667 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCAB46 3' end, mRNA sequence. CK245030.1 GI:39791186
                            911
                                                                                                          970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 GGAGAGCAAGAAAGAGTATGTGGGTTGGGTTCTTGATGACTGTGGTTGCAGCTCTTCTCTA 584
  852 TTCCTCTTTACTCTCTGGAATTATAGGCGCTTTTTTACTTCCTGTTTACGAAAGTTTTGGC
                                                                                                      CGCCTCCATTGTCATAGGGTTGCTCACAGGACTTGACAACTACTTATATTCTTACGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         465 TTTGTTGACGGTTGGTATCGGGATCCTTGCGTTACACAGTGATGAGACAAACCGGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AGCATATCTGCCAGTTTCAACTTCATCGCTCATAATCGGAACTCAACTAGCTTTCAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748 GCTTTTTGCTGTGCTTATAGTTAAACAGAAATTGACAGCGTATTCGACGAATTCCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 TCTCTTCGCTTTCTTGTTAGTCAAGCAAAGTTCACTCCGTTCTCCATAAACGCCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamida; Solanales; Solanaceae; Solanum.
1 (bases 1 to 868)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4113"
/clone="PDCAB46"
/tissue_trallus"
/lab_host="DH10B-TonA"
/clone_lib="potato callus cDNA library, normalized a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 263; DB 14;
Pred. No. 7.5e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
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Solanum tuberosum
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Best Local Similarity
Matches 450; Conserv
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CK245030/c
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                                                                                                                                            /note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 CGGTGGTCCTTTAATCTCTCGACTCTATTTCATTGACGCGCCAACGAATTTGGATACC 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 GARGGRIACTIAAACTCATGGGGACCCGCGAAATTACCCGTTTCAACTTCGACTCTAAT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATCGGAACTCAACTAGCTTTCAACGCTCTTCGCTTTCTTGTTAGTCAAGCAAAAGTT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 CAACGCGACTCAACTTGCGTTCACTGCGCTTTTTGCTGTGTTATAGTTAAACAGAATT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACAGCGTATTCGACGAGTTCCGTCGTTTTGCTTATCGCCGGAGCTGCGACTTTAGCTCT 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618 CAAGAAAGCTCGTCAAGAAATCACTTTCCCACTTGTGCTTGAGATTCAGATGGTCATGTG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  615 TATGAAGGCGAAGCAAGCTGTTACTTACACTACAGTATTGGAGATTCAGATGGTTTTGGG 674
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                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                   98
                                                /tissue_type="callus"
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/clome_lib="potato callus cDNA library, normalized and
full-length"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 CACTCCGTTCTCCATAAACGCCGTCGTTTTGTTGACGGTTGGTATCGGGATCCTTGCGTT
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                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                        Length 979;
                                                                                                                                                                                                                                                                          Pred. No. 3.4e-51;
0; Mismatches 381; Indels
                                                                                                                                                                                                                                                    22.3%; Score 273.4; DB 14;
57.8%; Pred. No. 3.4e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAACGCCGGAAATTCAAGG-------
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCBR86"
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                          Similarity
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885 AAGTGTTCTGCTTCCGGTGACTGAAGTTTTCGCCGTCGTTGTTTCCGGGAGAAGTTTCA 944
                                                                                                                                                                                                                                            271 CGCTTTTTACTTCCTGTTACCGAAGTTTTGGTGTAATTTTGTTCCACGGAAAATTTCA 212
                                                                                 825 CTTCTTAGGAGCCATAGGGATTGTGTTTTTGTGCATCATCACTAGCTTCTGGTGTTCTGAT 884
                                                                                                                                                                                                             331 GCICCIGGGGTIAGITGCAGITATITITIATICTICCTCTTTACTCTCGGAATTATAGG 272
628 CGAGTCCACGAAGGATTATATGTTGGGGTTTGTGATGACGTTTATACGGTGCGGTGTTATA 569
                                                 509
                                                                    645 CCCACTTGTGCTTGAGATTCAGATGGTCATGTGCCTTGCTGCTACTTTTTCTGTGTCAT 704
                                                                                                                                                   765 TGGAGGATCAGTGTTTTACTATGCATTGATAGTGATCACAGGAATAATATGGCAAGGTTT 824
                              585 IGCTITIAIATATACCCCTCGTIGAGCTAACTTACAAGAAAGCTCGTCAAGAAATCACTIT 644
                                           1005 CGAGTTTAAATCCGGCAAGAAAG 1027
                                                                                                                                                                                                                                                                                                                               151 TGAATATGAACAAGGAAGAAGG 129
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Search completed: September 25, 2004, 09:57:35 Job time : 3632 secs

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GGGATTGTGTTTTGTGCATCATCACTACTTCTGGTGTTCTGATAAGTGTTCTGCTTCCGGATTGTTTTGTGCTTCTGCTTCTGGTGTTCTGATAAGTGTTTCTGCTTCCG
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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AAACGAATCTGGTTCATGAGCTTCCTATCAACCGCTGGTTTTCCAATCATCCTCATCCCT
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Forsyth RA,
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
06-WAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                            ACA43388 standard; DNA; 729
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Trawick JD,
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Wall |
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   9901S-0149368P.
9901S-0149175P.
9901S-0149723P.
9901S-0149922P.
9901S-0149930P.
9901S-015066P.
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453; Conserv
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11-SEP-1999;

15-SEP-1999;

16-SEP-1999;

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24-SEP-1999;

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26-CT-1999;

13-CT-1999;

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26-0CT-1999;
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20-Aug-1999;
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25-Aug-1999;
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29-OCT-1999;
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Matches 453;
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polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation. (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibites cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibite proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound a activity; (11) a culture compound strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required cor collection of an organism. The antisense modeled for rational and all and all and an organism of the candidate molecules for regional
                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7%; Score 21; DB 7; Length 729;
100.0%; Pred. No. 7.8;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes 4b contig DNA sequence #747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 AAGATGAAGAATGGTTTGATA 310
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(CNRS ) CNRS CENT NAT RECH SCI.
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(first entry)
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Best Local Similarity 100.
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29-AUG-2002
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                         ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pot_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36971.
                                                                                                                                                                                                                                                            Gaps
               present invention relates to nucleic acid sequences (ABQ67188-
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                                                                                                                                                                                                                            DB 6; Length 2791; 7.5;
                                                                                                                                                                                                 Sequence 2791 BP; 942 A; 450 C; 622 G; 777 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                     705
                                                                                                                                                                                                                                                                                                        693 GCTACTTTTTCTGTGTCATT 673
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2000US-0225447P

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Claim 14; SEQ ID NO 3618; 180pp; French

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25-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-023499FP.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235367P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236399P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-023703P.
03-OCT-2000; 2000US-023937P.
20-OCT-2000; 2000US-024178PP.
20-OCT-2000; 2000US-024178PP.
20-OCT-2000; 2000US-024178PP.
20-OCT-2000; 2000US-024178PP.
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20-OCT-2000; 2000US-024178PP.
20-OCT-2000; 2000US-024180PP.
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20-OCT-2000; 2000US-024180PP.
20-OCT-2000; 2000US-024180PP.
20-OCT-2000; 2000US-024180PP.
20-OCT-2000; 2000US-024647PP.
08-NOV-2000; 2000US-024647PP.
08-NOV-2000; 2000US-024647PP.
08-NOV-2000; 2000US-024647PP.
08-NOV-2000; 2000US-024652PP.
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08-NOV-2000; 2000US-024652PP.
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                                                             2000US-0226868P
          14-AUG-2000;

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10-SEP-2000;

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08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
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17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024921P.
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17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-02593P.
17-NOV-2000; 2000US-02593P.
17-NOV-2000; 2000US-02598P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025188P.
06-DEC-2000; 2000US-025188P.
08-DEC-2000; 2000US-025188P.
08-DEC-2000; 2000US-025188P.
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05-JAN-2001; 2001US-0259678P
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 36971; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

C anino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

activity, and can be used in gene therapy and vaccine production. (I)

C proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (I) expression. For

cxample, they may be used to treat disorders associated with decreased

CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome

CC explession by rectifying of (I) by expressing inactive proteins or to

c upplement the patients own production of (I). Additionally, (I)

C supplement the patients own production of (I). Additionally, (I)

C polynucleotides may be used to produce the secreted (I), by inserting the

CC mocleic acids into a host cell and culturing the cell to express the

C protein. (I) proteins and polynucleotides may be used to prevent,

C diagnose and treat immune/haematopoietic-derived cells. AAK64703

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC cancers and cancer metastases of haematopoietic antigen genomic

C to AAK8764 represent human immune/haematopoietic antigen genomic

C represent sequences used in the exemplification of the present invention

Seguence 25392 BP; 7641 A; 4435 C; 4734 G; 8582 T; 0 U; 0 Other;

Gaps ö 4; Length 25392; 0; Indels Query Match
1.7%; Score 21; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches

Zyskind JW; Xu HH;

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the invention fractors of an interior actual compilating any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a proposession is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continued by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular contiferation or the activity of a gene in an operon required for proliferation or that has an acitivity against a biological pathway or that has an activity against a biological pathway or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, activity; (11) a culture comprising strains in which the extent or product is overexpressed or underexpressed; (12) determining the extent compound, activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the content of the strains is present in a culture or collection of strains; or (13) identifying proteins or screening for homologous nucleic acids required for encounted for fartional activity descending for homologous nucleic acids required for encounted for encounted for encounted for encounted for fartional actional actions of the strains is present in a culture compound.
                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence is one of the target
the sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than S. aureus, S. typhimurium,
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                                                                                                                                                                                                                                                                                                          invention relates to an isolated nucleic acid comprising any one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 20; DB 7; Length 1017; 00.0%; Pred. No. 24;
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                                                                                            Ohlsen KL,
Forsyth RA,
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                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 24401; 1766pp; English.
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Mismatches
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Carr GJ,
                       06-MAR-2002; 2002US-0362699P
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                                                                                            Zamudio C,
Trawick JD,
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100.0%; Fit
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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The present invention relates to an isolated polymucleotide, comprising CC polymorphisms in the human diphtheria toxin receptor, heparin-binding compidermal growth factor-like growth factor (DTR) gene. DTR gene is cotated on chromosome 542: The polymucleotide comprising polymorphisms cc in the DTR gene is useful in studying the expression and function of DTR, and in expressing DTR protein for use in screening candidate drugs to treat diseases related to DTR activity. The methods and haplotypes are useful in improving the efficiency and output of several steps in the cuseful in improving the efficiency and output of several steps in the cuseful in improving the efficiency and output of several steps in the care diseases are setful for determining if an individual has one of the cuseful for determining if an individual has one of the cuseful for studying expression of the DTR isogenes in vivo, for in vivo screening cand testing of drugs targeted against DTR protein, and for testing the efficacy of therapeutic agents and compounds for tumour growth, smooth cefficiacy of therapeutic agents and compounds for tumour growth, smooth cuseful byperplasia or atherosclerosis in a biological system. The present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and processing the present companies of DTR general and DTR general and processing the present companies of DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and DTR general and
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"This degenerate base represents polymorphic site,
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"This degenerate base represents polymorphic site,
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"This degenerate base represents polymorphic site,
useful for screening or expressing proteins for treating diseases related to DTR activity.
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                                                                     Claim 21; Fig 1; 66pp; English
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Matches 20; Conservative
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             New mucleotide polymorphisms in the human diphtheria toxin receptor, heparin-binding epidermal growth factor-like growth factor (DTR) gene,
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/note= "Polymorphic site, PS8"
[2416. .12488
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'note= "Polymorphic site, PS6"
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'note= "Polymorphic site, PS4"
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note= "Polymorphic site, PS5"
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/note= "Polymorphic
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eplace(938, A)
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11293. .12415
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Gaps

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cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                      WO200157182-A2.
                               Homo sapiens.
                                                                                                                                                                                                                                      -JUN-2000;
                                                                                                                                                            24-FEB-2000
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                                                                                                                                                                                                                                                                                                                                          New nucleotide polymorphisms in the human diphtheria toxin receptor, heparin-binding epidermal growth factor-like growth factor (DTR) gene, useful for screening or expressing proteins for treating diseases related to DTR activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphisms in the human diphtheria toxin receptor, heparin-binding epidermal growth factor-like growth factor (DTR) gene. DTR gene is located on chromosome 5q23. The polymorlectide comprising polymorphisms in the DTR gene is useful in studying the expression and function of DTR, and in expression and function of DTR, and in expression and function of DTR, and in expression and thoughton to treat diseases related to DTR activity. The methods and haplotypes are useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. The kit and method are useful for determining if an individual has one of the haplotypes or haplotype pairs. The transgenic animals are useful for studying expression of the DTR isogenes in vivo, for in vivo screening and testing of drugs targeted against DTR protein, and for testing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and testing of drugs targeted against DTR protein, and for testing the efficacy of therapeutic agents and compounds for tumour growth, smooth muscle hyperplasia or atheroscierosis in a biological system. The present sequence is human DTR gene allelic variant
                                                                                                    /*tag= h
/note= "This degenerate base represents polymorphic site,
PS8"
*tag= f
note= "This degenerate base represents polymorphic site,
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note= "This degenerate base represents polymorphic site,
                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to an isolated polynucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 6; Length 16488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                            Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 22; ive 0; Mismatches
                                                                                                                                                                                                                                                                                          Parks KE,
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 60-66; 66pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             869 CTTCTGGTGTTCTGATAAGT 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK68992 standard; DNA; 42738 BP
                                                                                                                                                                                                                                                                                         Koshy B,
                                                                                                                                                                                                                                                              (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                           16-APR-2001; 2001WO-US012302.
                                                                                                                                                                                                                                   14-APR-2000; 2000US-0197375P.
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                         12392
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                                                                                                                                                       WO200179233-A2
                                                                                      misc_feature
                                       misc feature
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2000US-0237037P.
2000US-0237038P.
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2000US-0239935P.
2000US-0239937P.
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17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
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2000US-0249297P.
2000US-0249299P.
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11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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-NOV-2000; 2000US-0246527P.
-NOV-2000; 2000US-0246528P.
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17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
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2000US-0246474P.
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2000US-0246478P.
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2000US-0246476P.
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2000US-0241787P.
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08-NOV-2000; 2
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08-NOV-2000; 2
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17-NOV-2000;
17-NOV-2000;
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29-SEP-2000;
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29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
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17-NOV-2000;
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01-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
25-SEP-2000;
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08-NOV-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

C amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseages associated with inappropriate (I) expression. For

C example, they may be used to treat disorders associated with decreased

CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome

CC explession by rectifying mutations or deletions in a patient's genome

CC cupters affect the activity of (I) by expressing inactive proteins or to

CC polynucleotides may be used to produce the secreted (I), by inserting the

CC polynucleotides may be used to produce the secreted (I), by inserting the

CC protein. (I) proteins and polynucleotides may be used to prevent,

CT diagnose and treat immune/haematopoietic-related diseases, especially

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC cancers from the present invention. AAK54912 to AAK54950 and AAM82169

CC represent sequences used in the exemplification of the present invention
                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou Q, Aux GW;
Madhaven E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42738 BP; 15539 A; 8490 C; 8408 G; 10301 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant; herbicide; weed; crop field; growth; development; gene; ds.
                                                                                                                                                                                      Disclosure; SEQ ID NO 23804; 3071pp + Sequence Listing; English.
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1.6%; Score 20; DB 4; Length 42738;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levin JZ, Patton DA, Mcelver JA, Budziszewski GJ,
Tossberg J, Wegrich Glover L, Ashby CS, Thomas CR,
Lewis S, Dunn J, Cates E, Law MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36375 AAGTATGAATAAATTTGAA 36356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. thaliana gene 60944 #SEQ ID 79.
                                                       Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB95081 standard; DNA; 435 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUL-2001; 2001US-0305806P.
20-FEB-2002; 2002US-0358416P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-2002; 2002WO-EP007929.
              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
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P-PSDB; ADB95082.
                                                                                         WPI; 2001-483426/52
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vegetation, comprises combining a polypeptide with a compound to be tested for the ability to bind to the polypeptide or inhibit the activity Identifying an herbicidal compound, useful for controlling undesirable Example 9; SEQ ID NO 79; 273pp; English. the polypeptide.

The invention relates to a method for identifying a herbicidal compound.

The method of the invention comprises combining a polypeptide having at least 90% identical to any one of 48 69-1008 residue amino acid sequences (designated as P1-P48), given in the specification, with a compound to be tested for the ability to bind to the polypeptide or inhibit the activity of the ability to bind to the polypeptide or inhibit the activity of the polypeptide, under conditions conductive to binding or inhibiting, respectively. Also disclosed is a method for killing or inhibiting the growth or viability of a plant by applying to the plant the herbicidal compound identified by the novel method, a chimeric construct comprising a promoter operatively linked to the nucleic acid molecule. The method and polypeptides are useful in secree and molecule. The method and polypeptides are useful in a screening assays to identify compounds that interact or inhibit the polypeptides, thus as potential herbicides to control undesirable comprising nucleotide sequences that encode proteins (even numbers between ADB95003) and ADB95097) isolated from Arabidopsis thaliana comprising nucleotide sequences that encode proteins (even numbers) between a ADB95009) are essential for plant growth and development

Sequence 435 BP; 130 A; 72 C; 122 G; 111 T; 0 U; 0 Other;

Gaps . 0 Score 19; DB 9; Length 435; Pred. No. 78; 0; Indels Mismatches 100.0%; Pre .68 19; Conservative Query Match Best Local Similarity Matches

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ABQ38560 standard; DNA; 524 12-JUL-2002 ABQ38560; RESULT 13

BP.

Oligonucleotide for detecting cytosine methylation SEQ ID NO 25151 (first entry)

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens

WO200218632-A2

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826.

(EPIG-) EPIGENOMICS AG.

Guetig Berlin K, Piepenbrock C, olek A,

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WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomelectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used:

(i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method in the Claim 12; 56pp + Sequence Listing; 56pp; German. disclosure of the invention

Sequence 524 BP; 26 A; 60 C; 174 G; 264 T; 0 U; 0 Other;

Gaps ö DB 6; Length 524; 78; 0; Indels 0; Mismatches Score 19; Pred. No. 100.0%; . 68 ; Query Match
Best Local Similarity 100.00
Best Local 19; Conservative

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1165 TGTGTGTTTTTGTTGT 1183 ч 셤 ઠ

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ABQ38561/c RESULT 14

BP. ABQ38561 standard; DNA; 524

ABQ38561;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 25152.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2.

07-MAR-2002.

01-SEP-2001; 2001WO-EP010074.

01-SEP-2000; 2000DE-01043826. 05-SEP-2000; 2000DE-01044543.

(EPIG-) EPIGENOMICS AG.

Berlin K, Olek A, Piepenbrock C,

ä

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.

Claim 12; 56pp + Sequence Listing; 56pp; German.

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            This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic convertance of the amplicon is hybridised to two classes, each with at least one member, convertance of bybridisation to both classes is determined from the label on degree of hybridisation to both classes is determined from the label on control standard. The method is used: coligomers, the degree of methylation is calculated. The method is used: coligomers, the degree of methylation is calculated. The method is used: coligomers, the degree of diseases, e.g. cancer, disorders of the central correvous, cardiovascular, gastrointestinal and respiratory systems etc., nervous, cardiovascular, gastrointestinal and respiratory systems etc., cand of a wide range of diseases, e.g. cancer, disorders of the central control in the control control in the control control in the method allows the method allows the method allows the method allows the method allows the method allows the method in the control control in the invention
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Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 524 BP; 264 A; 174 C; 60 G; 26 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 3385.
                                                                                                                                                                                                                                                                                                                                                                                               1.6%; Score 19; DB
Local Similarity 100.0%; Pred. No. 78;
les 19; Conservative 0; Mismatches
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21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999; 26-0CT-1999; 28-0CT-1999;

28-OCT-1999 29-OCT-1999

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Query Match 1.6%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 77, Matches 19; Conservative 0; Mismatches
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1 MKNGLIIINCIILTIGTCGG......DKPQPPETELPILPVSDYVA 356 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:*
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geneseqp2002s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		d			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
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-	1798	100.0	356	m	AAB10684	Aab10684 A. thalia
7	1792	99.7	356	Ŋ	ABB91157	Abb91157 Herbicida
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7	553	30.8	367	m	AAG22805	
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σ	553	30.8	382	m	AAG22804	
10	553	30.8	382	m	AAG40301	-
11	550	30.6	367	ო	AAG44536	
12	525	29.5	107	m	AAG15104	Aag15104 Arabidops
13	513.5	28.6	386	m	AAG52938	_
14	513.5	28.6	387	ო	AAG52937	7
15	513.5	28.6	394	m	AAG52936	9
16	512.5	28.5	386	m	AAG16270	0
17	512.5	28.5	387	m	AAG16269	σ.
18	512.5	28.5	394	m	AAG16268	80
19	497	27.6	303	ო	AAG44537	_
20	473.5	26.3	335	m	AAG17233	Aag17233 Arabidops
21	473.5	26.3	355	٣	AAG17232	7
22	473.5	26.3	361	m	AAG17231	н
23	449.5	25.0	250	m	AAG44538	8
24	445	24.7	358	ß	ABB93669	_
25	191	0.6	134	m	AAG16232	Aaq16232 Arabidops

	Aag2225 Arabidops Aae22124 Human 543 Ada20211 Sulphate Abb49383 Listeria Aag20806 Arabidops	Abb60159 Drosophil Abp25655 Streptoco Aab18970 Amino aci Abp97205 Tumour-as Aam93831 Human pol	Aam39861 Human pol Aab5714 Human pro Aam41647 Human pol Aag20807 Arabidops AdC96821 E. faeciu Aar54876 Human H13
AAU57026 ABM53545 AAG28227 AAG28226	AAG28225 AAE22124 ADA20211 ABB49383 AAG20806	ABB60159 ABP25655 AAB18970 ABP97205 AAM93831	AAM39861 AAB95714 AAM41647 AAG20807 ADC96821 AAR54876
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ALIGNMENTS

AAB10684 standard; protein; 356 AA. (first entry) A. thaliana PUP1 protein. 19-JAN-2001 AAB10684; RESULT 1 AAB10684

PUP1; transgenic plant; nucleobase transporter; apical dominance; flowering behaviour; senescence; pesticide distribution.

Arabidopsis thaliana.

24-AUG-2000.

DE19907209-A1

99DE-01007209 19-FEB-1999; 99DE-01007209. 19-FEB-1999;

(FROM/) FROMMER W.

Gillissen B, Buerkle L, Andre B, Frommer WB;

WPI; 2000-566202/53. N-PSDB; AAA97919 Nucleic acid, useful for producing transgenic plants with altered nucleobase transport, encodes a nucleobase transporter protein of Arabidopsis thaliana.

Claim 1b; Page 16-17; 24pp; German.

This invention describes a novel nucleic acid encoding a plant nucleobase transporter (1) (1) is produced by complementation of a nucleobase transport (NBT)-defective host cell with a plant gene bank by selection of NBT-positive cells. (1) is used to isolate homologous sequences from bacteria, fungi, plants, animals and humans, for expression of the exoded protein (11) in prokaryotic or eukaryotic cells, for inhibiting expression of (11) in prokaryotic plants have modified nucleobase transgenic crop plants. The transgenic plants have modified nucleobase transport properties, e.g. altered affinity and substrate specificity that may result in more efficient nucleobase transport properties, endicated affinity and substrate specificity that may result in more efficient nucleobase transport in leaves, changes in apical dominance, flowering behaviour and senescence, or improved distribution of pesticides. This sequence represents the Arabidopsis

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of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                        1 MKNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSR
                                                                                                                                                      1 MKNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSR
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                                                                                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequenc from plant with nucleic acid or amino acid sequences from non-plant
                                                                                        Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 367; 261pp + Sequence Listing; English.
                                                                                                                   Indels
                                                                                           99.7%; Score 1792; DB 5;
99.7%; Pred. No. 2.5e-191;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB91156 standard; protein;
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Best Local Similarity
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                                                                       Sequence 356 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising allguing and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor
                                                                                                                                                                              TQLAENALFAFLIVKQKFTPFSINAVVLJTVGIGILALHSDGDKPAKESKKEYVVGFLMT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
             thaliana PUP1 protein which is described in the method of the invention
                                                                                                                                                                 RRGNRNPNNAENKRKTKLFLMETPLF1ASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG
                                                                                                               1 MKNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSR
                                                                                                                               CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPILPVSDYVA 356
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                Length 356;
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                                                                                         Indels
                                                               Score 1798; DB 3;
Pred. No. 5.3e-192;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidally active polypeptide SEQ ID NO 368.
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0
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100.0%;
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                                                                                             356, Conservative
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                                                                               Similarity
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                                            Sequence 356 AA;
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28-APR-1999;
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04-MAY-1999;
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       240
                                                                                                                                                        RRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG 120
                                                                                                                                                                   TQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMT 180
                                                                                                                                                                                                  EAREFKIGGSVPYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVV 300
                                                                                                                                                                                                                                                                      1 MKNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSR 60
                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                        CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSG--KKVVDKPQPPETELPIL--PVSD 353
                                                                                                                                  WAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAR
                                                                                      63.1%; Score 1134.5; DB 5; Length 351;
59.9%; Pred. No. 8.4e-118;
ive 66; Mismatches 66; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 41941.
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99US-0123180P.
99US-01257848P.
99US-0126264P.
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99US-0128714P.
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                                                                                    Query Match
Best Local Similarity 59.9°
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                       Sequence 351 AA;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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26.0CT-1999;
06.0CT-1999;
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                                                                                                                                                                                                                                                                          179 MTVVAALLYARILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVI
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0
                                                                                                                                                                                                                        49.6%; Score 892; DB 3; Length 178;
llarity 99.4%; Pred. No. 4.5e-91;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 15224.
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99US-0123180P.
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23-MAR-1999;
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06-APR-1999;
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16-APR-1999;
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  14-OCT-1999)
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01 - JUL - 1999;
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                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                Gaps
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Matches 143, Conservative
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

Arabidopsis thaliana

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06-SEP-2000

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2000EP-00301439

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17-OCT-2000 (first entry)

AAG22805;

AAG22805 standard; protein; 367 AA

AAG22805

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Arabidopsis thaliana protein fragment SEQ ID NO: 49987,

Arabidopsis thaliana

EP1033405-A2

18-OCT-2000 (first entry)

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AAG40302

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termination sequence.
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                                                                                                                                           Length 107
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                                                                                                                                         Score 525; DB 3;
Pred. No. 2.5e-50;
0; Mismatches 1;
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99US-0160981P.
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99US-0161404P.
99US-0161405P.
99US-0161406P.
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99US-0123180P.
99US-012554P.
99US-012664P.
99US-0126785P.
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99US-0161992P.
99US-0161993P.
99US-0162142P.
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99.1%;
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                                                                                                                                               Best Local Similarity 99.1
Matches 106; Conservative
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21-0CT-1999;
21-0CT-1999;
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25-0CT-1999;
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09-MAR-1999;
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06-APR-1999;
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19-APR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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23-APR-1999;
23-APR-1999;
28-APR-1999;
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PR 22-JUL-1999; 99US-0145132P.
PR 23-JUL-1999; 99US-0145134P.
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PR 27-JUL-1999; 99US-0145214P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                               132 LLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKES----KKEYVVGFLMTVVAALLY
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                                                                                                                         Score 513.5; DB 3;
Pred. No. 2.7e-48;
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Matches 119; Conservative
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99US-0141287P.
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30-JUN-1999;
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71 12 ILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRGNRNPNNAE Gaps 15; Length 394; Indels Query Match
28.6%; Score 513.5; DB 3;
Best Local Similarity 35.1%; Pred. No. 2.8e-48;
Matches 119; Conservative 71; Mismatches 134; g 8

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187 162 222 131 132 LLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKES----KKEYVVGFLMTVVAALLY 72 NKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAF 163 FLASQKITPFILASYLLTISSTILVIQHEPESPSSTSKSAAKSKYVIGYICAVGSSAGY ď ò ठ 용

188 AFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKI 223 SLVLSLIDYAFEKILKKYTFKAILDMATYPSMVATCVVVVGLFGSGGWKKLSTEMEEFQL 307 QAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETE 345 용 셤 ò ਨੇ 8

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> completed: September 23, 2004, 23:47:12 He : 93 Becs Search compl Job time : 9

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Sequence 5663, Ap
Sequence 3104, Ap
Sequence 7104, Ap
Sequence 2108, A
Sequence 25058, A
Sequence 25058, A
Sequence 25058, A
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Sequence 5262, Ap
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-489-019A-9580

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US-09-328-35-7659

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US-09-134-000C-5123

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
Sequence 18070, A Sequence 7574, Ap Sequence 28655, A Sequence 6031, Ap Sequence 6026, Ap Sequence 4893, Ap Sequence 5563, Ap Sequence 12578, Ap Sequence 5355, Ap Sequence 5288, Ap Sequence 5288, Ap Sequence 5288, Ap Sequence 5288, Ap Sequence 5288, Ap Sequence 5055, Ap Sequence 5055, Appli
                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 2, Appli
Sequence 2922, Ap
Sequence 10571, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7110
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Maggachugetts
                US-09-489-039A-7574
US-09-134-000C-631
US-09-134-000C-631
US-09-543-681A-6026
US-08-677-049-11
US-09-134-001C-4519
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US-09-489-039A-10571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...376

SEQUENCE DESCRIPTION: SEQ ID NO: 6448:
18-09-107-532A-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6448, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 376 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6448:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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; Sequence 8, Application US/08132990A
; Sequence 8, Application US/08132990A
; Patent NO. 58345B-6
; GENERAL INFORMATION:
APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKAYUKI
TITLE OF INVENTION: Human Retrovirus Receptor and DNA Coding Therefor
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 LLVSFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 STSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKB----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7%; Score 121; DB 2; Length 629;
23.6%; Pred. No. 0.00058;
                                            229 MFIVGDFKVIAREAREFKIGGSVFY----YALIVITGIIWQGFFL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Mismatches 112;
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REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8105-004-999
TELECOMMINICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TIPE: TADEN CIGNETIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,990A
FILING DATE: 07-0CT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/084,729
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05569
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/899,075
FILING DATE: 11-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/627,950
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-JUN-1992
RATIOR APPLICATION DATA:
APPLICATION NUMBER: 07/806,178
FILING DATE: 13-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.6%;
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Best Local Similarity 23.6
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                            RESULT 3
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILIAGION NUMBER: US 60/117,747
PRIOR PILIAGION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
                                                                                            15;
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                  6.8%; Score 122.5; DB 4; Length 376;
19.7%; Pred. No. 0.00021;
ative 55; Mismatches 123; Indels 115; Gaps
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                                                                                                                                                                      69 NAENKRIKLFLMETPLFIASIVIGLITGLDNYLYSYGLAYL
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9580
Query Match
Best Local Similarity 19.,.
The 72; Conservative
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ETDIP 376
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US-09-489-039A-9580
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Sequence 7659, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7659
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Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: GTC99-0398; CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04
    513 V------TVLGREALTKGALWAVFLLAGSALLCA--VVTGVIWRQ------PESKT 554
                                                                                               280 SLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLW---GFVSYF-YGEFKSGKKV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 ILENIQGYSFQKPIKLVLTQAETASDENPV---KVVLG-----KYLWGSSMLWLCCFTS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 SLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLL-----TVGIGILALHSDGDKPAK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: | | :: | | :: | 270 LLV-----FYLLTSWMPTILKTAGFSTQQFSLIAAIFPFGGVIGATIMGWYMDKLNPTT 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 ESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVI 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.5%; Score 116; DB 4; Length 45
Best Local Similarity 19.3%; Pred. No. 0.0012;
Matches 65; Conservative 54; Mismatches 127; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : | : | : | | : | 410 LSLSGIFFILAIPTFISFIALSLKVIYEKSKHKQVL 445
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SEQ ID NO 4974
LENGTH: 419
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                                                                                 227 IGMFIVGDFKVIAREA-----REFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCAS 279
                                                                                                                                                                                                  113 STSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKR---- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 IGMFIVGDFKVIAREA------REFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCAS, 279
                                                                                                                                                                         280 SLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLW---GFVSYF-YGEFKSGKKV 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 STNDSQLGFLPEAEMFSLKTILSP-----KNMEPSKISGLIVNISTSLIAVLIIT-FCI 512
SKKBYVVGFLMTVVAALLYARILPLVELTYKKARQEITFPLVLEI--OMVMCLAATFFCV 226
                                                                                                                             513 V-----TVLGREALTKGALWAVFLLAGSALLCA--VVTGVIWRQ-----PESKT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 LLVSFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 SKKEYVVGFLMTVVAALLYARILPLVELTYKKARQEITFPLVLEI--QMVMCLAATFFCV 226
                         74;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application PC/TUS9209382
GENERAL INFORMATION:
APPLICANT: MERUELO, DANIEL
APPLICANT: YOSHIMOTO, TAKATUKI
TITLE OF INVENTION: Therefor
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES:
B CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DB 5; Length 629; 0.00058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 121; 23.6%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09382
FILING DATE: 19921213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shuwel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: MERUELO=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-5197
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 amino acida
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 23.6
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                            336 VDKPQ 340
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613 LDADQ 617
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PCT-US92-09382-8
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169
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Sequence 7116, Application US/09543681A

Sequence 7116, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-09
PRIOR PLING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INFORMATION:
TITLE OF INFORMINON: BUTERCOCCUGUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUTERCOCCUGUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BUTERCOCCUGUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 103796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5123
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AREFKIGGSV--FYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTE-VFA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 RGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 QLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 VAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIARE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 KRSGATDMIRLICWVSLVPPLPLLALSYLFEGP-----QAIERAVLNMSWGG--FGALL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 OSGVLLAIČSY1LWGIT--PLFYRL--LPGAOPLELLAORLIWSIPLLLUVRLF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 6.3%; Score 113.5; DB 4; Length Local Similarity 21.5%; Pred. No. 0.0015; hes 69; Conservative 52; Mismatches 147; Indels
                                               257 IVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFA 298
                                                                                        219 YIAFGATTVGFAIWSFLLRHYPASLVTPFALAV--PVSGMLA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; sequence 5123, Application US/09134000C; Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 VFLFHEAFDAVKGVSFSL-IW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 VVCFREKFQAEKGVSLLLSLW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Proteus mirabilis
US-09-543-681A-7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-134-000C-5123
                                                                                                                                                                                               US-09-543-681A-7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCHICANGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 101196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKARQEITFPLVLEIQMY--MCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYAL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAF 189
                                                                                                                                                                                                                                                                                                                                                                                                             257 BFTHASPTFITF-----MLVLIGVGFSIGNHLGGRFADLSINKTLIGFLVLLIVMM---- 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 ILPLVELTYKKARQEITFPLVLE-----IQMVMCLAATFFCV--IGMFIVGDFKVIARE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 A-----REFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSIASGV-LISVLL 291
                                                                                                                                                                                                                              70 AENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALF 129
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                                                                                                                                                                                               13 LTIGTCGG-PLLTRLYFTNGGKRI-WFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPN-N 69
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                                                                                                         DB 4; Length 419;
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                                                                                                                                                      Indels
                                                                                                         ; Score 115.5; DB 4;
; Pred. No. 0.0013;
47; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27266, Application US/09252991A Patent No. 6551795
                   ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4974
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                                                                                                              Query Match
Best Local Similarity 24.2%;
Matches 73; Conservative 47
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Best Local S:
Matches 65
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210 · - VLEIQMVMCLAATFFCV - IGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGF 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2%; Score 112; DB 4; Length 51 20.3%; Pred. No. 0.0038; ive 47; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5385
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Proteus mirabilis
US-09-543-681A-5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.2%
Best Local Similarity 20.3%
Matches 61; Conservative
                                                                                                                                                  319 WGFVSYFYG 327
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346 TFLLLYFFG 354
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US-09-107-532A-5693
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn boucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
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                                                                                                                                                                                                                                                                                                                   ---SLVQGMPLDANGNMHAQFT----DYFNLFSIVGGVALTLLCYLHGMNYIALKTEG- 192
                                                                                                                                                                                                                                                                                                                                                                                       193 -PIRERARNYAEILYGVLYIGLVVFAVLMY-------FKTDFYEKNFAVTL---IL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 TLAIVVLTVIAN--VGVFK--RKEMLAFLASG----LTLVVLVALLESGLFPRVMIGSEG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 YKSRIVAYF---TTSLLAGGASMIMVLPAVLDLRTNGETLSEITTFKTEATAFLDIIMKN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 GIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEITFPL-- 209
                                                                                                                                                    55 --VSFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLFV 112
                                                                                                                                                                                                                                                                               113 STSSLIIGTQLAFN----ALFAFLLVKQKFTPFSINAVVLLTV-----GIGILALHSDGD 163
                                                                                                                                                                                                                                                                                                                                                        164 KPAKESKKEY---VVGFL---MTVVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                218 CLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGFF----LGAIG 273
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; Pred. No. 0.0047;
54; Mismatches 121; Indels 117; Gaps
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                                                                                                                             11 IILTIG-----TCGGPLLTRLYFTNGGKRIWFMSFLSTAGPPIILIPLL----
                                                                                           Gaps
                                                    Query Match 6.3%; Score 113.5; DB 4; Length 342; Best Local Similarity 23.8%; Pred. No. 0.0016; Matches 82; Conservative 52; Mismatches 99; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 FDLLIKDATSTPYTLKIMTWISLSILPFVLPYT-AWSYYIFRKR 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 ---IVFCASS-----LASGVLISVL---LPVTEVFAVVCFREK 305
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
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; ORGANISM: Enterococcus faecalis US-09-134-000C-5123
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 20.9
Matches 77; Conservative
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US-09-134-000C-4997
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Sequence 5385, Application US/09543681A

Batent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
FILE REPERENCE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                 268 FLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKG------VSLLLSL 318
                                                                                                                          303 EXDDLGVL-----SGLILILL----AIFALA------MGTKGATSYTYVTLTSFVLTA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 LIPLSQSLLLN-----NYPPAKRNMALALWSVTIVVAPILGPILGGYISDNYHWGW-I 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AYLPVSTSSLIIGTQLAFNALFAFILVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FFINVPFGVLII---MCISNTLAGRETKTEIKPIDTIGLVLLVVGVGALQIMLDQGKELD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 AATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCAS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 SLAS---GVLISVLLPVTE------VFAVVCFREKFQAEKGVSLLLSLW 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 LIPLLVSFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGL--DNYLYSYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 ESKKEYVVGFLMTVVAALLYAFIL------PLVELTYKKARQEITFPLVLEIQMVMCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YEGTIVLLPLLLÖEVF----GYTATWA
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32397
LENGTH: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 TFFCVIGMFIVG----DFKVIAREAREFKIGGSVFYYALIVITGII--WQGFFLGAIGIV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 LYLC---EFYLGATSHAVSVFADPALNATNGGOIFSRYVDALFGSVGTW---LMG--GIV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 PLFIAS---IVIGLLTG------LDNYLYSYGLAYLPV-----STSSLIIGTQLAFNA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 L------MTVVAALLYAFILPLVELTYKKARQEITFP-----LVLEIQM--VMCLAA
                                                                                                                                                                                                                                                                                                                                                                                                               45 FOSGNO--WFSTSL---GFLVTGVLLPFLTLVTVAIRGRGER-------LSIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 LFAFLLVKQ-----KF-TPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVV-GF
                                                                                                                                                                                                                                                                                                                                                                     28 FINGGKRIWFMSFLSTAGPPI--ILIPL--LVSFLSRRRGNRNPNNAENKRKTKLFLMET
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1 Similarity 22.1%; Pred. No. 0.0065;
74; Conservative 42; Mismatches 98; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                                                              ; Score 111.5; DB 4; Length 463; ; Pred. No. 0.0037; 45; Mismatches 99; Indels 95
TITLE OF INVENTION: DIAGNOSTICS AND THERAI FILE REFERENCE: 2709:1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32397
                                                                                                                                                                                                                                                                                        Query Match 6.2%;
Best Local Similarity 26.0%;
Matches 84; Conservative 46
                                                                                                                                                                                                                      ; ORGANISM: Proteus mirabilis US-09-543-681A-8204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-32397
                                                                                                                                                       SEQ ID NO 8204
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Best Local S
Matches 74
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; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 GDKPAKESKKEYVVGFLMTVVAALLYAFIL-PLV----ELTYKKARQEITFPLVLBIQ 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 MVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGF----FLG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 -----TFFQMLGEYILDGFHVAITVAAML-----IGFVALIAMINAIFHGIFGIFGE 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.2%; Score 111.5; DB 4;
Best Local Similarity 20.3%; Pred. No. 0.0031;
Matches 64; Conservative 55; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 IIINCIIL--TIGTCGGPLLTRLY--------
                                                                                             COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
CORENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun.1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40.489
REFRENCE/DOCKET NUMBER: GTC-012
TELECHMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELERAX: (781)893-6277
INFORMATION FOR SEQ ID NO: 5693:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...402

; SEQUENCE DESCRIPTION: SEQ ID NO: 5693:

US-09-107-532A-5693
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                                                                        MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 PIVFISAIIGILR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 402 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AIGIVFCASSLASGV 285
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         COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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13; 130

84; Indels

41; Mismatches

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56 SLTFL:-----IGFAQGLTAGLAIITAQRYGAKDYRGLKKSFAASVVISLVVTVIL 106
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                                                                                                                                                                                                                               131 ---FLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEY----VVGFLMTVVA 183
                                                                                                                                                                                                                                                                                                                                                                                          184 ALL-YAFILPLVELTYKKARQEITPPLVLEIQMVMCLAATFFCVI--GMFIVGDFKVIAR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 TVLSLLFIRPMLQLMQ------TPPEILD-----QAQTFISIILLGIFASVSFNLLSN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 EAREFKIGGS---VFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPV-TEV 296
                                                                                 77 KLFLMET-PLFIASIVIGLITGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFA---
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        Conservative
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59;
    Matches
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
    480 ARLRRILERIGRLPDGWAGRLELPADESDGTSLLRQILGAELRGGTLLLWATFFWGLLII 539
                                                                                                                                                              540 YLLIN-----BAATISAMFQLGGT 572
                                                                                                                                                                                                                                                                                                                                                                                                               210 VLBIQMVMCLAATFFCVIGMFIVGDFKVIARBAREFKIGGSV----FYYALIVITGIIWQ 265
                                                                                                                                                                                                                                                            153 IGILALHSDGDK--PAKESKKEYVVGFLMTV-VAALLYAFILPLVELTYKKARQEITFPL 209
                                                                                                         GLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QVGANALAADFYPTRSRATGVSW- 652
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                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 GFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...457
SEQUENCE DESCRIPTION: SEQ ID NO: 5465:
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REGISTRATION NUMBER: 40,489
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5465:
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TYPE: amino acid
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STATE: Massachusetts
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Best Local Similarity
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US-09-107-532A-5465
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Best Local S:
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Sequence 174205,
Sequence 45872,
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1331.366 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB_Dep:*
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| cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB_Dep:*
| cgn2_6/ptodata/2/pubpaa/USOO_PUBCOMB_
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-437-963-186454
US-10-437-963-1864544
US-10-424-599-245361
US-10-424-599-249885
US-10-437-963-193908
US-10-437-963-146343
US-10-437-963-146343
US-10-437-963-14206
US-10-424-599-14526
US-10-424-599-14526
US-10-425-114-45875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349238 seqs, 321558718 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB E
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Sequence 144907, Sequence 104380, Sequence 174935, Sequence 12131, Sequence 218003, Sequence 218003, Sequence 2185383, Sequence 204152, Sequence 204152,	38370 40564 25777 35609 26129 37550 26399	equence 2 equence 1 equence 6 equence 1 equence 4, quence 35	Sequence 35, Appl Sequence 35, Appl Sequence 7, Appli Sequence 90, Appl Sequence 198415,
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ALIGNMENTS

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TYPE: PRT
ORGANISM: Oryza Bativa
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ORGANISM: Glycine max
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Sequence 216343, Application US/10424599

Publication No. US20040031072A1

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Avoid to David K

APPLICANT: Applicant: Acou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 285684

LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 VVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAR 240
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                                                              265 GGFFLGAIGIVFCASSLASGVLISVLLPVTEVPAVVCFREKFQAEKGVSLLLSLWGFVSY
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Best Local Similarity 62.6%; Pred. No. 4.8e-84;
Matches 186; Conservative 43; Mismatches 61; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_37387C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(306)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                292 FYGEIKQDRE-KNKNRCPETDLP 313
                                                                                                                              FYGEFKSGKKVVDKPQPPETELP 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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LOCATION: (1)..(3
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US-IU-43/-963-160022, Application US/10437963

Sequence 160022, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: La Roya, Yihua

APPLICANT: Bould K.

APPLICANT: Bundarov, Andrey A.

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APPLICANT: Bundarov, Andrey A.

APPLICANT: Bundarov, Andrey A.

APPLICANT
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFRENCE: 38-21 [53313] B
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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ilarity 48.0%; Pred. No. 5.9e-75;
Conservative 67; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Indels
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Best Local Similarity 56.9%; Pred. No. 3.4e-79;
Matches 169; Conservative 60; Mismatches 57; I
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Matches 169; Conserv
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Sequence 245361, Application US/10424599

Publication No. US20040031072A1

GRNERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION NUMBER: US 1010/424,599

CURRENT APPLICATION NUMBER: US 1010/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 245361
                            323 PQ-SGKLSYVMTLLWTAISWQVASVGVVGLIFVVSSLFSNVISTLALPIIPVFAVIFPHD 381
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245 FKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
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31.3%; Score 562.5; DB 12; Length 362;
Best Local Similarity 36.4%; Pred. No. 3e-47;
Matches 120; Conservative 67; Mismatches 130; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_63592C.1.pep
US-10-424-599-245361
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                      382 KMDGVKIIAMLMAIWGFMSYGHQLYVDGKK 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 KONGVKIISMLLALWGFASYIYONYLDDSK 346
                                                                                           305 KPQAEKGVSLLLSLWGFVSYFYGEFKSGKK 334
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                    | :||||||||||||:|| 96 RRREVEDDGAGAGAAATPLFILIMTPRILIVASAVVGLMTGVDDLLYAYGLAYLPVSTSSILI 155
                                                                                                                                                                                                                           156 STQLAFTAAFALLIVRQRFTAFSVNAVVILSVGAAMLGMNAGGDRPAGVSRAQYCAGFAM 215
                                                                                                                                                                                                                                                                                                                     120 GTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLM 179
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                                           KNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRR
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US-10-437-963-184544
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Publication No. US20040123343A1
GENERAL INFORMATION:
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Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Best Local Similarity 36.1%
Matches 119; Conservative
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US-10-437-963-184544
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156 AFTAVFAFLFVGLRFTPFSANAVVLLTVRERVRGRRCKTVRDPHDRGGWHLVDVQQVVTL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQL 123
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                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 37.1%; Pred. No. 1.3e-46;
Matches 132; Conservative 62; Mismatches 125; Indels 37;
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                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_90000C.1.pep
US-10-437-963-193908
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LOCATION: (1)...(391)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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APPLICANT: Zhou, Yihua
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APPLICANT: Zoo, Yongwei
APPLICANT: W. Wei
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APPLICANT: Bunkharov, Andrey A.
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                          APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 239885
LENGTH: 409
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37.1%; Pred. No. 1.3e-46;
tive 69; Mismatches 124; Indels 14; Gaps
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OTHER INFORMATION: unbure at all Xaa locations
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Best Local Similarity
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US-10-424-599-239885
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NAME/KEY: unsure
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APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBNCE: 38-21(53221) B CURRENT FILLE OF INVENTION NUMBER: US/10/437,963 CURRENT FILLE DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 136993
               La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Oryza sativa
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
FILE REFERENCE: 201(5321)B
CURRENT APPLICATION UNDER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
:|:||:|| |||||||||| : :|: ||:|-||:|| || || : || : ||:||:|| || || || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : |
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                                                                                                             MIVVAALLYAFILPLVELTYKKAR---QEITFPLVLEIQMYMCLAATFFCVIGMFIVGDF 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLJIGTQLA 124
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_46977C.1.pep
US-10-437-963-146343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 146343, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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US-10-437-963-136993
; Sequence 136993, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                      :|:
QVM 259
                                                                                                                                                                                                                                                     236 KVI 238
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LENGTH: 751
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                          124 AFNALFAFILVKOKFTPFSINAVVLLTVGIGILALHS--DGDKPAKESKKEYVVGFLMTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 ARBFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 LARWDLSPAA-YWAVLAALVATWQACLMGTAGMVYLTSSLHSGVCMTAVLTANVIGGVVV 301
                                                                                                                                                                                                                                                                72
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                                                                                                                                                                                                                                              182 VAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIARE
                                                                                                                                                                                                       5 LIIINCIILTIGTCGCPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRGN
                                                                                          Length 372;
                                                                                    Query Match 29.6%; Score 532; DB 16; Length 3 Best Local Similarity 36.8%; Pred. No. 3.4e-44; Matches 123; Conservative 67; Mismatches 122; Indels
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; PEATURE:

; OTHER INCOMMATION: Clone ID: PAT_MRT3847_128327C.1.pep

US-10-44-599-174206
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38519C.1.pep
US-10-437-963-136993
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Publication No. US20040031072A1
GENERAL INFORMATION:
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182 VAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIARE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ATTFE-GGRSAYYLVIIWGAITFQLGUAGTAIIFLGSTVLAGVLNAVRTPITSIAAVIL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 LLVLSILAMLVAFPASSILSRVYYDNGGQSKWIISWVAVAGWPLTALILFP--VYFIS-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 RGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGT 121
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249 GSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQA 308
                      259 GKASYLLNLTFTAILWQVFTIGCLGDISEVSSLFSNAISALGVPIVPMLAVLFFHDKMDG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.7%; Score 516; DB 12; Length 36 34.2%; Pred. No. 1.3e-42; tive 73; Mismatches 124; Indels
                                                                       309 EKGVSLLLSLWGFVSYFYGEFKSGKKVVDK---POPPETELPI 348
                                                                                                 319 IKGISMVLAIWGIVSYVYQQYLDDTKSENRNTTSHVPKASSPI 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_128326C.1.pep
US-10-424-599-174205
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LOCATION: (1)..(363)
OTHER INFORMATION: unsure at all Xaa locations
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iSequence 45872. Application US/10425114
Publication No. US20040034888A1
GENERAL INFORWATION:
APPLICANT: Liu, Jingdong
APPLICANT: Law, Vihua
APPLICANT: Kovalic, David K.
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Matches 114; Conservative
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERRENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 TKLFLMETPLFIASIVIGLITGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVK 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 SSASI----LAFIXVSIGLILALDCYLYSVGLWDLFVSTYSLICSSQLAFNAFFSYFLNS 139
                                                                                                                                                                                                                                                                                                                      182 VAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIARE 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CGGP--LLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRK 75
                                                                                                                                                                         62 RGNRNPNNAENKRKIKLFLMETPLFIASIVIGLLIGLDNYLYSYGLAYLPVSTSSLIIGT 121
                                                                                                                                                                                               122 QLAFNALFAFLLUVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTV 181
                                                                                                                                                                                                                                                                   265 ATTEK-GGRSAYYLVIIWGAITFOLGVLGGTAVIFLGSIVLAGVLNAVRTFITSIAAVIL 323
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                                                                                                                        42 LIALSILAMLVAFPASSILSRVYYDNGGSKMIISWVAVAGWPLTALILFP--VYFIS--
                                                                                                   S LIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFP---IILIPLLVSFLSRR
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                                                                   Gaps
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                              29.6%; Score 531.5; DB 12; Length 355; 35.0%; Pred. No. 3.6e-44; vative 73; Mismatches 120; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.9%; Pred. No. 3.7e-43;
Matches 123; Conservative 66; Mismatches 133; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_102285C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 145366, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                     Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                      Similarity
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61

Gaps

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us-09-5

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Tabaska, Jack B

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53113)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NOS: 73128

SEQ ID NO 45872

TYPE: TENOTH: 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.6%; Score 514; DB 12; Length 379;
Best Local Similarity 34.2%; Pred. No. 2.2e-42;
Matches 114; Conservative 73; Mismatches 124; Indels 22; Gaps
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ORGANISM: Glycine max
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September 23, 2004, 23:40:51; Search time 15.0847 Seconds (without alignments) 1228.856 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-913-767-8 1798 1 MKNGLIIINCIILTIGTCGG......DKPQPPETELPILPVSDYVA 356 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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46 45 47 PIILIPLLVSFLSRRRGNRNPNNAENKRKTKL-----FLMETPLFIASIVIGLLTGLDN 100

1 MKNGLIIINCIILTIGTCGGPLLTRLYFTN---GGK------RIWFMSFLSTAGF

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Query Match
8.0%; Score 144; DB 1; Length 311;
Best Local Similarity 19.1%; Pred. No. 0.0032;
Matches 73; Conservative 68; Mismatches 113; Indels 128; Gaps

O05256 bacillus su						
MAEN_BACSU	NU2M OENBE NU4M TRIRU	YRBG_ECOLI YS10_ARCFU	PTSB_PASMU YL31_ARCFU	YC61_METTH MVIN_BORBU	SP5B_BACSU POTC_MYCGE	ALIGNMENTS
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311 AA.	pdate) update) 1 S'region (ORPY).	Clostridiales; Clostridiaceae;		STRAIN=DSM 555; MEDLINE=96146540; PubMed=8550525; Soebling B., Gottschalk G.; "Molecular analysis of the anaerobic succinate degradation pathway in Clostridium kluyveri.";	<pre>/8:871-880(1996). LOCATION: Integral membrane protein (Probable). Belongs to the eamA transporter family.</pre>	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	VUF6. Transport; Transmembrane. POTENTIAL.	
PRT;	Created) Last sequence update) Last annotation update) protein in cat1 5'regi	dia; Clo		525; aerobic	al am2	right I	Tt; Transm POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL.	
STANDARD;	, Creat , Last , Last rt prot	kluyveri. rmicutes; Clostridia;	534; M.N.A.	STRAIN=DSM 555; BODLINE=96146540; PubMed=8550525; Sochling B., Gottschalk G.; "Molecular analysis of the anaero Clostridium kluyveri.";		This SWISS-PROT entry is copyright. It is postween the Swiss Institute of Bioinformatiche European Bioinformatics Institute. The mase by non-profit institutions as long amodified and this statement is not removed. Settings requires a license agreement (See lor send an email to license@isb-sib.ch).	EMBL; L21902; AAA92345.1; IIICETPYO; IPROU0620; DUF6. Pfam; PF00892; DUF6; 2. IRANSMEM 33 53 IRANSMEM 70 90 IRANSMEM 123 143 IRANSMEM 123 143 IRANSMEM 123 143 IRANSMEM 123 143 IRANSMEM 123 143 IRANSMEM 124 264 IRANSMEM 244 264 IRANSMEM 244 264 IRANSMEM 244 264 IRANSMEM 265 285 IRANSMEM 265 285 IRANSMEM 265 285 IRANSMEM 265 285 IRANSMEM 265 285	•
IT 1 CLOKL YCAY CLOKL P38943;	1995 1995 2003 tical	Clostridium kluyveri. Bacteria, Firmicutes; Clostridium.	NCBI_TaxID=1534; [1] SEQUENCE FROM N.A	STRAIN=DSM 555; BOBLINE=96146540; PubMe Soehling B., Gottschalk "Molecular analysis of Clostridium kluyveri.";	J. Bacteriol. 17 -!- SUBCELLULAR -!- SIMILARITY:	This SWISS-PROT between the Sw the European to use by non-pr modified and th entities requir	EMBL; L21902; AAA92345 IIICETPC; IPR000620; Dfam; PF00892; DUF6; 24 ITANSMEM 33 53 ITANSMEM 70 90 ITANSMEM 123 143 ITANSMEM 123 143 ITANSMEM 125 175 ITANSMEM 123 143 ITANSMEM 124 264 ITANSMEM 244 264 ITANSMEM 244 264 ITANSMEM 265 285	
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263 IWQGFFLGAIGIVFC-----ASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLL 315
                                                                                                                                                    ---NPAKVMEGIGGSRDLIGICFALVAAVVWSLYTVI----SKKRIELYGGYVFN---- 188
                                                                                                                                                                                     217 MCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITG------I 262
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                                               YLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHS 160
                                                                                                                                                                                                                                                                                  Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.; Gloning and sequencing of a 35.7 kb in the 70 degree-73 degree region of the Bacillus subtilis genome reveal genes for a new two-component system, three spore germination proteins, an iron uptake system and a general stress response protein.";
                                                                     BG
161 DGDKPAKESK----KEYVVGFLMTVVAALLYAFILPLVELTYKKARQEITFPLVLEIQMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=168 / Marburg;
MEDLINE=97074649; PubMed=8917076;
Schoeck F., Dahl M.K.;
Schoeck F., Dahl M.K.;
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals
"Analysis of DNA flanking the treA gene of Bacillus subtilis reveals
genes encoding a putative specific enzyme IITre and a potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto H., Uchiyama S., Sekiguchi J.;
"Cloning and sequencing of a 40.6 kb segment in the 73 degrees-76 degrees region of the Bacillus subtilis chromosome containing genes for trehalose metabolism and acetoin utilization.";
Microbiology 142:3057-3065 (1996).
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P39794; 034771;
P39794; 034771;
P30794; 034771;
P307954; 034771;
P307955 (Rel. 31, Last sequence update)
P507956 (Rel. 32, Last annotation update)
P507959 Probable PTS system, trehalose-specific IIBC component (EIIBC-TRE)
Component) (FC 2.7.1.69) (EII-TRE).
TREP OR TREB OR BSU07800.
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MEDLINE=98044033; PubMed=9384377;
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MEDLINE=97417488; PubMed=9272861;
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Becuillet S., Bruschi C.V., Coldwell B., Capuano N., Catter R. A. Capuano N., Catter R. A. Capuano N., Catter R. Chois S.K., Coldwell B., Capuano N., Catter R. Chois S.K., Catter N., Catter S. P., Emilia B. D., Emmeraon P.T. R. Beninger D., Catter S. C., Emilia R., Calleron N., Ching S.Y., Catter R. C., Pitter M., Pitter R., Calleron N., Ching S.Y., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R., Catter R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGFFLGAIG-- 273
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    Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Batrison D., Hoang L., Kasqle P., Lumm W., Pothler B., Olu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pletrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                             Transport; Transmembrane; Complete proteome
                                                                                                   deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the eamA transporter family.
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4296C7890CB91B7F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.3%;
                                                                                                                                                                                                                                                                                                              InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 21.3
1es 77; Conservative
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168
197
223
264
289
                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                    C69212; C69212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GE 328
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                                                                                                                                                                                                                                                                                                                                            Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 APITLLLTGFASFI-IIGPITFAIGNVLTSGLISVFGSFAALGGLLYGGFYSALVITGMH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                            153 WADLANMINLIAGTAFTFLPALIGWSAVKR----FGGNP--LLGIVLGVMLVHPDLLNAM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SLASGVLISV 289
                                                                                                                                                                                                                                                                                                                                                                                             NMNPLORAVKTLADIPI---PILPAIVTAGLLMGINNILTAEGIPF---STKSIVQVYPQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 LEIQMVMCLAATFFCVIG--MFIVGDF---KVIAREAREFKIGGSVF--YYALIVITGI- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLPVTE--VFAV-VCFREKF--------QAEKGVSLLLSLWGFVSYFY 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LIIGTQLAF-NALPAFLLVKQKFTPFSINAVVLLTVGIGILALHSD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDKPAKESKKEYV------VGFLMTVVAALLYAFILPLVELTYKKARQE-ITPPLV
                                                                                                                                                                                                                                                                                                                                                                     64 NRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSS-----
                                                                                                                                                                                                                                                                                                                                            Gaps
PS01035; PTS_EIIB_CYS; 1.
ansferase system; Sugar transport; Transferase;
krane; Inner membrane; Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                       59; Mismatches 112; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                      PHOSPHORYLATION (BY SIMILARITY) POTENTIAL.
                                                                                                                                                                                                                                                                                                              DB 1; Length 470;
                                                                                                                                                                                                                                                                                   7A741850A2697D53 CRC64;
                                                                                                                                                                                                                                       F -> S (IN REF. 1).
M -> L (IN REF. 1 AND 5)
A -> G (IN REF. 1 AND 5)
                                                                                                                                                                                                                                                                                                             Score 141; DB 1
Pred. No. 0.0073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical transport protein MTH841.
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                                                                                                                                                                                                                                                                                                                                         87; Conservative
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123
163
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                 ransferase
                                                                                                                                                                                                                                                                                   470 AA;
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                                                                                                                                                                                                                                                                                SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 FLMETPLFIASIVIGLLTGLDNYLYSYGLA------YLPVSTSSLIIGTQLAF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 NALFAFLLVKOKFTPFSIN----AVVLLTVGIGILALHSDGDKPAKES---KKEYVVGFL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 ILLVSTLGY------LVYVVVARLFNVSGWSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 AREAREFKIGGSVF-----YYALIVITGIIWQG--FFL----GAIGIVFCASSLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complementation cloning identifies CDG-IIC, a new type of congenital disorders of glycosylation, as a GDP-fucose transporter deficiency."; Nat. Genet. 28:73-76(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVVAALLYAFILPLVELTYKKARQEITFPLVLEIQM/MCLAATFFCVIGMFIVGDFKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANT CDG-IIC CYS-147. MEDLINE-21225289; PubMed-11326279; Medline-21225289; PubMed-11326279; Mid M.K., Eckhardt M., Gerardy-Schahn R., Vestweber D.; Inche K., Wild M.K., Inche Geretive in leukocyte adhesion deficiency II encodes a putative GDP-fucose_transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS CDG-IIC CYS-147 AND ARG-308. MEDLINE-21225290; PubMed-11326280; Luebke T., Marquardt T., Etzioni A., Hartmann E., von Figura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.9%; Score 124; DB 1; Length 287; 20.7%; Pred. No. 0.07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Indels
                                                                                                                                                                                                                                                                                            PIR; G69766; G69766.—
SubtiList; BG11066; ycxE.
IIICETPO; IPR004673; RhaT.
TIGRPAMS; TIGRO0776; RhaT: 1.
Hypothetical protein; Sporulation; Complete proteome.
SEQUENCE 287 AA; 30892 MW; E0FF3B0B47EBC56A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 GVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GIVISTL-----GGIFILREKKTKRQLIAIAIGI 270
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ID FCT1 HUMAN STANDARD;
AC Q96A29; Q9BV76; Q9NUJ8;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2004 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
TISSUE=Mammary gland, and Placenta;
                                                                                                                                                                                                                      EMBL; Z99106; CAB12200.1; -.
EMBL; M23547; -; NOT_ANNOTATED_CDS.
EMBL; M12276; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                              EMBL; D50453; BAA09023.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP-fucose transporter 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RX MEDLINE-98044033; Dubmed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Bourstier L., Brans A., Braum M., Brignell S.C., Bron S.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,

RA Choi S.K., Codani M., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rosport G., Rey M., Reynolds S.,

RA Setoguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Setouri M., Tamakoshi A., Taramakoshi A., Tarepstra P., Targeneger T.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

RA The complete genome sequence of the Gram-positive bacterium Bacillus
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J. Bacteriol. 166:238-243 (1986).
-- I- DBVELOPMENTAL STACE: Expressed during sporulation (By similarity).
-- SIMILARITY: TO A SIMILAR ORF IN B.MEGATERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                            "The 25 degrees-36 degrees region of the Bacillus subtilis chromosome: determination of the sequence of a 146 kb segment and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 272-287 FROM N.A.
MEDILINE=86168021; PubMed=3082854;
Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.;
"Characterization of the developmentally regulated Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJURE-89033889; PubMed=3141376; MEDIJURE-89033889; PubMed=3141376; Rather P.N., Moran C.P. Jr.; Compartment-specific transcription in Bacillus subtilis: "Compartment-specific transcription of the promoter for gdh."; J. Bacteriol. 170:5086-5092(1988).
                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                             P404<u>7</u>0; P94429;
01-FEB-1995 (Rel. 31, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                  287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97124189; PubMed=8969502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 113 genes.";
Microbiology 142:3047-3056(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                    Yamane K., Kumano M., Kurita K.
                                                                                                                                                                           Hypothetical protein ycxE. YCXE OR BSU03920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
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                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the nucleotide sugar transporter family
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai P., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatua Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transport; Sugar transport; Transmembrane; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R -> C (IN CDG-IIC).
/FTId=VAR 012347.
T -> R (IN CDG-IIC).
/FTId=VAR 012348.
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EMBL, AK027394; BAB55080.1; --
EMBL, AK002182; BAB452126.1; ALT_INIT.
EMBL, BC001427; AAH01427.2; --
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87 IASIVIGLLTGLDNYLYSY-GLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINA 145
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                                                                                                                                                                                                                                                                                                                                                                    228 WRLTFYNNVNACILFLPLLL-------LLGELQAL----RDFAQLGSA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      265 HFWGMMTLGGLF--GF---AIGYV-----TGLQIKFTSPLTHNVSGTAKACAQTVLAV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
High-afflnity cationic amino acid transporter-1 (CAT-1) (CAT1) (System Y+ basic amino acid transporter) (Ecotropic retroviral leukemia receptor homolog) (ERR) (Ecotropic retrovirus receptor homolog).
                                                                                                                                                                                                               120 LSVVFIGMIT-FNNLCLKYVGVAFYNVGRSLTTV-----FNVLLSYLLLKQ-----TTSF
                                                                                                                                                                                                                                                                                                                                            196 --LT-YKKARQEITF-PLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSV
                                                                                                                                                                                                                                                                                                                                                                                                                              252 FYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTE------VFAV
                                                                                                                               Gaps
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"Identification of three cationic amino acid transporters in
placental trophoblast: cloning, expression, and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Membr. Biol. 171:55-62(1999).

-!- FUNCTION: High-affinity, low capacity permease involved in the transport of the cationic amino acids (arginine, lysine and ornithine) in non-hepatic tissues. May also function as an ecotropic retroviral leukemia receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Urinary bladder;
MEDLINE-92217962.
Albritcon L.M., Bowcock A.M., Eddy R.L., Morton C.C., Tseng L.,
Albritcon L.M., Cavalli-Sforza L.L., Shows T.B., Cunningham J.M.;
Farrer L.A., Cavalli-Sforza L.L., Shows T.B., Cunningham J.M.;
The human cationic amino acid transporter (ATRC1): physical and
genetic mapping to 13012-914.";
Genomics 12:430-434(1992).
                                                                                                                               74;
                                                                                  'Match 6.8%; Score 123; DB 1; Length 364; Local Similarity 23.8%; Pred. No. 0.1; les 68; Conservative 49; Mismatches 95; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 VCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 LYYEETKSFLWWTSNWMVLGGSSAYTWVRGWEMKKTPEEPSPKDSE 358
                        BAA92126).
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"Molecular cloning and characterization of a novel human ghomologous to the murine ecotropic retroviral receptor.";
Virology 185:10-17(1991).
49 49 W -> S (IN REF. 4).
258 258 F -> L (IN REF. 3; BAA921.
364 AA; 39808 MW; 2E659D49C5C5E92E CRC64;
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MEDLINE=99415840; PubMed=10485994;
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MEDLINE=92024065; PubMed=1718082;
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                                                                                                                                                      SKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEITFPLVLEI--QMVMCLAATFFCV
                          SINDSQLGFLPEAEMFSLKTILSP-----KNMEPSKISGLIVNISTSLIAVLIIT-FCI
                                                                 227 IGMEIVGDFKVIAREA-----REFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCAS
                                                                                      280 SLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLW---GFVSYF-YGEFKSGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
Ltoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horiuchi T.;
A S70-kb DNs sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypotherical transport protein ydhP.
                                                                                                                                                                                                                                                                                                                            389 AA.
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EMBL; D90809; BAA15423.1; -.
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EcoGene; EG13950; ydhP.
InterPro; IPR007114; MFS.
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. . ) (POTENTIAL)
N-LINKED (GLCNAC. . ) (POTENTIAL)
                          -i- TISSUE SPECIFICITY: Ubiquicous.
                                                                                                                                                                                                                                                                                                                            MIM; 104615; -.
GO; GO:005887; C:integral to plasma membrane; TAS.
GO; GO:0005887; C:integral to plasma membrane; TAS.
InterPro; IPR004293; AA/rel_permease.
InterPro; IPR004841; Permease region.
Pfam; PF00324; aa_permeases; Z.
PIGRFAMS; TIGR00966; ZA0303; 1.
TIGRFAMS; TIGR00966; ZA0303; 1.
Transmembrane; Glycoprotein; Transport; Amino-acid transport;
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717734D4793647C5 CRC64;
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                 SUBCELLULAR LOCATION: Integral membrane protein.
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EMBL; X57303; CAA40560.1; --
EMBL; AF078107; AAC27721.1; --
PIR; S29685; S29685.
Genew; HGNC:11057; SLC7A1.
MIM; 104615; --
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629 AA;
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                                                                                                                                                                                                                                                                                                                                                                             83 TPL-FIASIVIGLL--TGLDNYLYSYGL----AYLPVSTSSLIIGTQLAFNALFAFLLVK 135
                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repressor-encoding gene (scrR).";
Gene 101:45-50(1991).
-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The ICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phosphor-HPT); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                         54 TPLIFGVGVVSGLFWAVGQSNQLKSIDLIGVSKTMPIST-----GLQLVSTSLFGVIVFH
                                                                                                                                                                                                                                                                                  136 QKFTPFSI----NAVVLLTVGIGILALHSDGDKPAKESKKEY------VVGFLMTV
                                                                                                                                                                                                                                                                                                      182 VAALLY----AFILPL-----VELTYKK-----ARQEITFPLV-----LEIQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTS system, sucrose-specific IIBC component (EIIBC-SCR) (Sucrose-permease IIBC component) (Phosphotransferase enzyme II, BC component) (EC 2.7.1.69) (EII-SCR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blatch G.L., Scholle R.R., Woods D.R.; "Nucleotide sequence and analysis of the Vibrio alginolyticus sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    histidine + Sugar phosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Contains 1 PTS EIIB domain.
-!- SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 PKVGVATSFSLSQMGIVISTLGGIIILGEKKTKRQLVGIIIGIILIIIAGVM
                                                                                                                                                                                                                                                                                                                                                                                                                             216 VMCLAATFFCVIGMFIV----GDFKVIAREAREFKIGGSVFYYALIVITGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence and analysis of the Vibrio alginolyticus
                                                                                                                                       Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales;
Vibrionaceae, Vibrio.
                                                                                                                                                                            Indels
                                                                                   Hypothetical protein; Sporulation.
SEQUENCE 286 AA; 30490 MW; 95AB89D02511D74D CRC64;
                                                                                                                                                                          79;
                                                                                                                                       Query Match
6.6%; Score 119; DB 1;
Best Local Similarity 27.2%; Pred. No. 0.15;
Matches 63; Conservative 34; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AA
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MEDLINE=91285433; PubMed=2060795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
15-MAR-2004 (Rel. 43, Last ann
                               PIR; 139851; JS0384.
InterPro; IPR004673; RhaT.
TIGRFAM8; TIGR00776; RhaT; 1.
                EMBL; D90043; BAA14098.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uptake-encoding region.";
Gene 95:17-23(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatch G.L., Woods D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio alginolyticus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91071601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 YVVGFLMTVVAALLYAFILPEVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGM--- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||: :|: |: ||| || || :| :| :| :| :| -- vGYQGSVLPVLVVSAFILAKVELGLRKVIPSVLDNLLTPLLAIPIAGLLTFTVVGPFTR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 VKQKFT---PFSINAVVLLTVGIGILALHSD------GDKP-----AKESKKE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 PLFIASIVIGLITGLDNYLYSYGLAYLPVSTSSLIIG----TQLA-----FNALFAFIL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 PIIPAIVAGGLLMGIYNLLTAQGLF---IDGKSLİEANPGLTDLANMINTFANAPFVYLP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 ILLAFSASKKFGGNP--YLGAALGMLMVHPDLLNGWGFGGASVSGNIÞVWNILGFEIQK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

STRAIN-0157:H7 / EDL933 / ATCC 700927;

STRAIN-0157:H7 / EDL933 / BURGet J. Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpariick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpariick H.A.,

Grofbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Abelch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
4Npothetical transport protein ydhP.
Whp OR 22679 OR EC52366.
Bacterichia coli 0157-147.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriales; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                      26 26 PHOSPHORYLATION (BY SIMILARITY)
324 324 PHOSPHORYLATION (BY SIMILARITY)
479 AA; 49890 MW; FBF906B5170E3EB7 CRC64;
                                                                                                                        EMBL; M76768; AAA27555.1; -.

R PIR; J00781, J00781.

R HSSP; P05053; JIBO.

R INCEPTO; JPR001996; Ptrans_EIIB.

R INCEPTO; JPR001996; Ptrans_EIIB.

R INCEPTO; JPR001996; Ptrans_EIIC.

R INCEPTO; JPR001719; PTSIIC_GJC.

R PÉam; PF00367; PTS_EIIB; J.

R PCDODM; PD001476; FTS_EIIB; J.

R TIGRRAMS; TIGR00826; EIIB gJC; 1.

R TIGRRAMS; TIGR00826; EIB gJC; 1.

R PROSITE; PS01035; PTS_EIIB CYS; 1.

R PROSITE; PS01035; PTS_EIIB_CYS; 1.

R PROSITE; PS01035; PTS_EIIB_CYS; 1.

R PROSITE; PS01035; PTS_EIIB_CYS; 1.

R PROSIDE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 118; DB 1; Length 479; 28.4%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FIVGDFKVIAREAREFKIGGSVF--YYALIVITGI 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licens@@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 -----TPVFVTAMLVL-IGVGFSIGNYLGGKLADKSVNGTLKGFLL-----LLMVIM 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 LPLVELTYKKARQEI-----TFPLVLEIQM-VMCLAA-----TFFCVIGMFIVGDFK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 LAIPPLARNKEGAAISMAVWGAAIFAVVPPLQMRVMRVASEAPGLSSSVNIGAFNLGN-- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 NKRKIKLFLMETPLFIASIVIGLL-TGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 FLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 LTIGTCGG-PLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 LTLANIGGVPAATWLGETIG----WRMSFLATAGLGVISMVSL--FFSLPKGGA---GAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genome sequence of enterohemorrhagic Scherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                         (Potential).
-!- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50850; MFS; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane; Complete protein; Transport 7 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 VIAREAREFKIGGSVFY----YALIVITGIIWOGFFLGAIGIVFCAS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B53864327068881E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Pred. No. 0.3;
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.5%; Score 116.5;
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InterPro; IPR005828; Sub_transporter.
Pfan; PF00083; sugar_tr; 1.
[2]
SEQUENCE FROM N.A.
SERGIN-CO157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11259796;
                                                                                                                                                                                                                                                                                                            EMBL, AE005389, AAG56646.1; -. EMBL, AP002558, BAB35789.1; -. PIR, B85773, B85773.
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64
91
1121
1151
1180
224
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71
101
131
160
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267
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389 AA;
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Best Local &
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425 ------LAITIFSFVGIPPLVGFFAKQMVLSAALD---NGYIFLTLIAILTSVIGA 471
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InterPro; IPR006153; Na H porter.
InterPro; IPR004709; NaH exchang.
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Transmembrane; Glycoprotein; Tr
                                                        266 GFFLGAIGIVF 276
                                                                                                              472 VYYĽNIÍKKIF 482
                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 LVLBIQMVMCLAATFFCVIGM-FIVGDF--KVIARBARBFKIGGSVFYYALIVITGIIWQ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNYLYSYGLAYLPVSTSSLII----GTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 TQFRIKRLLAYSTISHVGFILLALSGCSIESTQAFIFYLIQYSISNLNV-FIIIITIGFS 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 LYGYIT-----TNKEYKDLLDKNNSPIQVISQLKGYFYINPLLSLS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cummings D.J., McNally K.L., Domenico J.M., Matsuura B.T.; "The complete DNA sequence of the mitochondrial genome of Podospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genet. 17:375-402(1990).
CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cummings D.J., Domenico J.M.; "Sequence analysis of mitochondrial DNA from Podospora anserina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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EMBL; X14485; CAA32646.1; -.
PIR; S02154; S02154; S02154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154; SO2154;
                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'vasiveness of a class I intron in three separate genes."; Mol. Biol. 204:815-839(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane.
-!- SIMILARITY: Belongs to the complex I subunit 2 family.
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                                                                                                                                 01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoreductase chain 2 (RC 1.6.5.3).
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                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
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                                                  556 AA
                                                  PRT;
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MEDLINE=90291512; PubMed=2357736;
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                                                  STANDARD;
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                                                                                                                                                                                                                                                           Podospora anserina.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pervasiveness of
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLETE GENOME.
                                                                                                                                                                                                                                                                                           Mitochondrion.
                                               NU2M PODAN
P15578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Nucleated erythrocyte;

X MBDINEs-2325712; Pubmed=1379718;

BOTGES F., Sardet C., Cappadoro M., Pouyssegur J., Motais R.;

BOTGES F., Sardet C., Cappadoro M., Pouyssegur J., Motais R.;

Cloning and expression of a cAMP-activated Na+/H+ exchanger:

T "Cloning and expression of a cAMP-activated Na+/H+ exchanger:

T evidence that the cytoplasmic domain mediates hormonal regulation.";

Proc. Natl. Acad. Sci. U.S.A. 89:6765-6769(1992).

- I- PUNCTION: Involved in pH regulation to eliminate acids generated by active metabolism or to counter adverse environmental conditions. Major proton extruding system driven by the inward sodium ion chemical gradient.

- SUBCELLULAR LOCATION: Basolateral membrane.

- I- FUNCTION: Activated by cAMP, protein kinase C.

- I- MISCELLANEOUS: Inhibited by amiloride and 5-amino-substituted derivative and activated in a cooperative fashion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport; Antiport; Sodium transport;
                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Na(+)/H(+) exchanger beta (Na(+)/H(+) antiporter) (Beta-NHE).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neoprerygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the Na(+)/H(+) exchanger family.
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EXTRACELLULAR (POTENTIAL).
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M3 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
M7 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                      132 CLLPPIILDAGYFLPIRPFTENVGTILVFÄVI---GTLWNAFFWGGLLYALCQIESVGLS 188
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                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                          72 EIALWILLALLMKLGFHLIPRLSAVVPESCLLIVVGLLVGGLIKVIGEEPPVLDSQLFFL
                                                                                                                                                                                        146 VVLLITVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEI
                                                                                                                                                                                                                                      206 TFPLVLEIQMVMCLA------ATFFCVIGMFIVGDFKVIARE------
         ------AREFKIG-GSVFYYALIVITGIIWQGFFLGAIGIVFC-----
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; PubMed=7542800;

Relachmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                     83; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: May play a role in L-lactate transport.
                                                                                                                                                                                                                                                                                                                                                                         -----EVF-AVVCFREKFQAEKGVSLLLSLWGFVSYFYGBFKSGKKVVD 337
                                                                                                                                                                                                                                                                                                                                                                                      249 SKVGTVTVLDVFLGVVCF---FVVSLGGVLVGAIYGFLAAFTSRFTSHTRVIE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                             6.3%; Score 113; DB 1; Length 759;
19.5%; Pred. No. 0.94;
tive 41; Mismatches 83; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Forencial).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Putative L-lactate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                         57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
   352
372
376
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446
467
759
648
                                                                                                                            759 AA;
                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LSRRRGNRNPNNAENKRKTKLFL-----METPLFIASIV------IGLLTGLDN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 YLYSYGLAYLPVSTSSLIIGTQLAFNALF-----AFLLVKQ----KFTPFSINAVVLLT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 VGIGILAL------HSDGDKPAKESKKEYV---VGFLMTVVAALLYAFILPLVE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 TTLGSLGLFEISKGLIFSLKNIFGSNVSSSYKLLYVPALIPFVITVLIA-----IPFFK 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 LIYKKARQEITPPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 ISSSNVKQ----ILVSSLQQ---SKNPFIALIGALVMVMLMLVGGEHSMVKIIGRTF--- 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 LIVITGIIWQGF--FLGAIGIVFCASSLASGVLI-SVLLPVTEVFAVVCFREKFQAEKGV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIMNSVPVSFGAVGTPTWFGFGALKLSEDMILEIGSITAFIHSIAALIIPLLALRILV-- 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.2%; Score 111; DB 1; Length 53
21.3%; Pred. No. 0.95;
tive 56; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56884 MW; F3C1DF47E54217FB CRC64;
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                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003804; Lactate perm.
Pfam; PF02652; Lactate perm; 1.
TIGRFAMS; TIGR00795; lctP; 1.
                                                                                                                                                                                                                                      EMBL; U32801; AAC22871.1; -. PIR; H64110; H64110.
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Best Local Similarity
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508
532 AA;
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TRANSMEM 23
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                                                                                                                           Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borrises R., Bourslier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Fabret C., Ferrari E., Foulger D.,
RA Ghims Y., Colasi D., Rabret S., Galizzi A., Galleron N.,
RA Ghims Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
Allibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Couris B., Karamata D., Kasabara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Nuback M.,
RA Kutita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
RA Resecan B., Purnelle B., Ropee M., Sadaie Y.,
RA Rieger M., Rivolta C., Roche B., Roche B., Rose M., Sadaie Y.,
Schowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Rosero, M., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Sato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wadler B., Moseles M., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997).
-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the eamA transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 110.5; DB 1; Length 330; 18.9%; Pred. No. 0.68;
                  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7C6C65F1EDB276B5 CRC64;
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POTENTIAL
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InterPro; IPR000620; DUFG.
Pfam; PF00892; DUF6; 2.
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                                                                                  106 ICLLÝGVQÝTTGTESGILTSTTPMLIGILSFFLLREKIEKKTLIGILLAVCGVMAINLFG 165
                                                                                                                          161 DGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLA 220
                                                                                                                                                                     -----LSPHISALAI 208
48 KLMVERIPVFLSSGLRFLIASVVLLMLFCIEKGFPALTKKDVFVLLVQSFTGV--FLFS 105
                                          ----YGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHS 160
                                                                                                                                                                                                                                                     209 STFVSLFGFLFFLPFALFEASSFDYSVPTVLDWSYVLYYALFVTV----LAFYLWYSGVT 264
                                                                                                                                                                                                                                                                                                276 FCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLWG-FVSYFYGEFKSGKK 334
                                                                                                                                                                                                             221 ATFFCVIGMFIVGDFKVIAREAREFKI-----GGSVFYYALIVITGIIWQGFFLGAIGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Prictohman J.L., Weidman J.F., Small K.V., Sandusky W., Fuhrmann J.L., Wichtchman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Moyayen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M. Tomb J.-F., Dougherty B.A., Bott K.P., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                           265 KVPAGV-SGIFTSVLPVSAVILSGVILKEPFEFVHFIGIACVIGGIFVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 107-215 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE=94075230; Pubmde=8253680;
PEterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Complete proteome.
                                                                                                                                                                   166 AG---SQDGTPHALFGNMLIIAAVIGEALFTLMAKL-----
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01-OCT-1996 (Rel. 34, Last sequence update)
8-EFB-2003 (Rel. 41, Last annotation update)
Hypothetical protein MG447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
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169 LHYNLDQSSFEQNFQANSFQQFFNKKAIDVASBYVYILIGL-NIIPMLSRLFFYLAQSE- 226
                                                                                                                                                                                                                                                                                     118 IIGTQL------AFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAK 167
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                                                                                                                                                                                                                                                                                                                                                     224 FCVIGM---FIVGDFKVIAREAREFKIG------GSVFYYALIVITGIIWQGFFLGAI 272
                                                                                                                                                                                                                                                                                                                                                                                                                                     273 GIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSL----WGFVSYFYGE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 AI----SNLASAAIFGELQGVRTVSSYKFGQKKYDEIKKINIYTVIICISFGSLIYLLTA 413
                                                                                                                                                                                                     109 IVLINAINIFIPLGTGVIFSKAIGRNDQNKIQEAWNTGLISTTVFGLITQFLVLSFAKEW 168
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                                                                                                                                                              91; Gaps
                                                                                                                                    Query Match 6.1%; Score 110.5; DB 1; Length 547; Best Local Similarity 19.8%; Pred. No. 1.1; Matches 73; Conservative 64; Mismatches 140; Indels 91;
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Search completed: September 23, 2004, 23:50:21 Job time : 19.0847 Becs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 23, 2004, 23:42:01 Run on:

1; Search time 24.8588 Seconds (without alignments)
1362.072 Million cell updates/sec

US-09-913-767-9 Title: Perfect score:

1760 1 MVKALVIINCIILAIGNCGG......QDESQETEQSSLSRFISEC 352 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
[: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	I ID Description	: C86408 F3H9.12 protein -	B84749 hypothet	D86408	hypothetical pro	T04922 hypothetical	D96506 hypothetical	T04923 hypothetical	A84634 hypothetical	T04921 hypothetical	C85087 hypothetical	G86330 hypothetical	D96613 unknown prote	H96516	E96516		H86232	D84597 hypothetical	T10557 hypothetical	B97305 probable cat:	I39989	AC1252	B75159	D71181 hypothetical	B83384 conserved hyp	F83698	AI1614	F72219 conserved	- Franker
	Length DB	351	356	356	344	1128	379	348	315	358	432	393	390	392	389	398	383	323	368	461	518	345	287	292	296	311	345	288	000
dp	Query Match I	99.1	65.3	64.1	31.7	31.6	31.6	31.6	30.1	28.6	27.0	20.3	16.0	15.9	15.8	14.9	•	8.0	•	7.6	7.6	7.6	7.5	7.4	7.3	7.3	7.3	7.2	
		1744.5	1149	1128	557.5	557	5:955	555.5	530	502.5	475	357	282	279.5	277.5	262.5	261.5	140.5	134.5	134	134	133.5	131.5	130	129	129	129	•	101
	Result No.		7	Э	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	ac

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AE1193	802154	C82368	C69212	A83677	C95147	A98015	F86772	T50265	E83355	A72487	G70007	AF2944	D98338	T17144	T17166
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348	556	295	343	457	292	296	313	374	450	311	369	426	426	459	459
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	125.5 7.1				_	_	120 6.8	_						118 6.7	

ALIGNMENTS

RESULT 1

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.20-Mar-2001 #sequence_revision 02-Mar-2001
C;Accession: G6408
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, B16-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Liu, Z.A.; Luros, J.S.; Malti, E.; Kim, C.C.C., L.; J.H.; Y.; Liu, X.K.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G6408
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A;Residues: 1-351 <STO>
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A;Residues: 1-351 <STO

C; Genetics

A;Map position: 1 C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70

1; Gaps Query Match 99.1%; Score 1744.5; DB 2; Length 351; Best Local Similarity 99.7%; Pred. No. 3e-125; Matches 351; Conservative 0; Mismatches 0; Indels 1;

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9 9 1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR 1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR 셤 ਨੇ

61 RRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI 120 61 RKSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI ò 셤

121 AIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVM 180 ò

121 AIFSFFMVKHKFTPFTINAVVLLTVGAAVLGWHTETDKPVHETHKQYITGFLITVAAAVM 180 g

181 YAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREF

ò

240

120

239 300 241 KLGEALFYVVAVFSAIIWQFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKF 181 YAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFK-ALPKEAREF g ò

301 QAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISEC 352

240 KLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLDITEVLAVIFYHEKF 299

a

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hydrothetical protein T9A21.70 - Arabidopsis thaliana hydrothetical protein T9A21.70 - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C;Accession: T04924
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Submitted to the Protein Sequence Database, February 1999
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A;Accession: T04924
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A;Residues: 1-344 <BEV>
A;Cross-references: EMBL:AL021713
A;Cross-references: EMBL:AL021713
C;Genetics: C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEAREFKLGEALF-YVVAVFSALIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAV 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MUID:21016719; PMID:11130712
A,Accession: D86408
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-356 <STO>
A,COSS-references: GB:AE005172; NID:g9795614; PIDN:AAF98412.1; GSPDB:GN00141
A,Molphanian: 1
A,Map position: 1
C,Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 VCFREKFQAEKGVSLLISLWGFVSYFYGEFKSG--KKVVDKPQPPETELPIL--PVSD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 ILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRSNNVGDSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 SQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLIT
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31.7%; Score 557.5; DB 2; Length 344;
Best Local Similarity 35.3%; Pred. No. 4.1e-35;
Matches 120; Conservative 72; Mismatches 131; Indels 17
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                                                                                                                                                                                                                                                                                                                                                                            Query Match

64.1%; Score 1128; DB 2; Length 35

Best Local Similarity 60.1%; Pred. No. 2e-78;

Matches 215; Conservative 66; Mismatches 65; Indels
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A;Introns: 11/1
A;Note: T9A21.70
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D86408

D86408

Cipturine permease [imported] - Arabidopais thaliana
Cipturine permease [imported] - Arabidopais thaliana
Cipturine permease [imported] - Arabidopais thaliana
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                                                                                                                                                      hypothetical protein At2g33750 [imported] - Arabidopsis thaliana
hypothetical protein At2g33750 [imported] - Arabidopsis thaliana
C,Speciess Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001
E;B4749
E;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M; Koo, H; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Lie: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84749
A;Residue type: DNA
A;Residue type: DNA
A;Residue : 1-35 csTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QALPKEAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 LAVIFYHEKFOAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPIS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFK----- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKTVLVIINCIFLAIGNCGGPLAMARLYFQNGGERIWFPSFLQTVGCPLIFFPLLLSFLRR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: GB:AE002093; NID:g1707019; PIDN:AAC69140.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                               300 QAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISEC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.3%; Score 1149; DB 2; Length 356;
60.4%; Pred. No. 5.1e-80;
ive 68; Mismatches 57; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: up:necolory, C;Genetics:
C;Genetics:
A;Gene: At2g33750
A;Gene: At2g33750
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
C;Superfamily: Arabidopsis thaliana hypothetical protein 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 60.4
Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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ઠ 셤 ò 셤 ò 셤 ઠે 셤 ò 셤 ò g ò 셤 99

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Alathors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.: C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: D96506
A; Retaus: preliminary
A; Molecule type: DNA
A; Residues: 1-379 <STO>
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C;Date: 23-Apr-1999
S;Accession: T04923
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, February 1999
A;Reference number: 215390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 LSLMQPSFEKILKRETFSVVLEMQIYTSLVATCVSVIGLFASGEWR-TLHGEMEGYHKGQ 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 NVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 FFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEK 304
                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005173; NID:98655985; PIDN:AAF78258.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 LPLVELAYOKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 LYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNNVGDSTSFFLIKPR-LLIAAV
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A;Note: T9A21.60
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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A;Cross-references: BMBL:AL021713
A;Experimental Bource: cultivar Columbia; BAC clone T9A21
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.6%; Score 556.5; DB 2; Best Local Similarity 34.4%; Pred. No. 5.3e-35; Matches 115; Conservative 89; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 31.6%; Score 555.5; DB 2; al Similarity 36.7%; Pred. No. 5.8e-35; 120; Conservative 72; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 IMAMLIAIWGFASYVY---QNHIDDLKVRQARQQ 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 GLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQ 338
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Best Local Similarity
Matches 120; Conserva
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                                                                                                                                                                                                                                                                                                                                                           A; Gene: T12C22.2
                                                                                                                                                                                                                                                                                                                                    C, Genetics:
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                                                                                                      183 FRKVLKKQTFSEVINMIIYMSLVASCVSVVGLFASSEWK-TLSSEMENYKLGKVSYVMNL 241
                                                                                                                                                                                                     242 VWTAVTWQVFSIGCTGLIFELSSLPSNAISALGLPVVPILAVIIFHDKWNGLKVISMILA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    905 TAFFSYFLNSQKFTPLIVNSLFLLTVSSALLVVNTDSENTTNVSRVQYVIGFICTIGASA 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEARE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 FKLGEALPYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEK 299
                                                                         YQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVA 251
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31.6%; Score 557; DB 2; Length 1128;
Best Local Similarity 36.1%; Pred. No. 1.4e-34;
Matches 125; Conservative 76; Mismatches 131; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 FOAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSL
                                                                                                                                                                                                                                                                       312 LWGFVSYFY-----GEIKSGEDKRRIQQEESQE 339
                                                                                                                                                                                                                                                                                                            A,Molecule type: DNA
A,Residues: 1-1128 <BEV>
A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar Columbia; BAC clone T9A21
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A;Introns: 76/2; 402/1; 526/3; 762/1
A;Note: T9A21.50
                                                                            192
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hypothetical protein AT4g08700 [imported] - Arabidopsis thaliana (c)Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: C85087
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Ttle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Accession: C85087
A;Accession: C85087
A;Actus: preliminary
A;Atatus: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <STO>
                                                                                                                                                                                 C;Accession: T04921
S.Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, February 1999
A;Reference number: 215390
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                                                                                hypothetical protein T9A21.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGBAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.6%; Score 502.5; DB 2; Length 358; Best Local Similarity 33.2%; Pred. No. 6.4e-31; Matches 113; Conservative 80; Mismatches 120; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 60/3
A;Note: T9A21.30
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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A;Accession: TOGG:1
A;Molecule type: DNA
A;Residues: 1-358 <BEV>
A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar Columbia; BAC clone T9A21
C;Genetics:
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Matches 103; Conserva
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
Cispecies: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
Cispecies: 03-Feb-2001 #sequence_revision 02-Feb-2001
Ridin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Nature 402, 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A846424
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 - STO>
A,Residues: 1-315 - STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPPLVELAYQKAK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 IWOGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLALSLWGFV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 MDMIIYVSLVASCVSVVGLFASSEWK-TLSSEMDNYKHGKVSYIMNLVWTAVTWQVFSIG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AIGLIFSTSSLVSGIMISVL-LPITEVLAVIFYHEKFQAEKGLSLALSLWGFVSYFYGE- 322
                                                                                                80 VLGLLVGADCYLYSIGLLYLPVSTYSLICASQLAFNAFFSYFLNSQKLTPIILNSLFLLT 139
                                                                                                                                                                                 145 VGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPLVELAYQKAKQTMSYTLV 204
                                                                                                                                                                                                                        140 ISSTILAFNNEETDSTKVTKGEYVKGFICTVAASAGYGLVLSLQQLAFLKVLKKQNFSEV 199
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                                                                                                                                                                                                                                                                                                            LEFQLILCLIASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLG 264
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VYYDNGGNSKWLATVVQLVGFPVLLPYYILSFKTHATTDRDGKRTS-----PRNRVLVYV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g24220 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 16-Feb-2001
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C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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10 LLSRLYFSNGGKSKWIISWVAVAGWPITCLILLPTYI---
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30.1%; Score 530; DB 2; I
Best Local Similarity 35.5%; Pred. No. 4.6e-33;
Matches 117; Conservative 71; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 SYFYGEIKSGEDKRRIQQEESQETEQSSLS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDDKNLKKNHEITTTESPDPPEAEEST 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 ----IKSGEDKRRIQQEESQETEQSS 344
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A;Gene: At2g24220
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Unknown protein T15M6.24 [imported] - Arabidopsis thaliana G'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thalian. 02-Mar-2001 #text_change 31-Mar-2001
C'Accession: D96613
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MulD:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H95516
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 PLVALFVVLARDFRMDDERSWPRIGTLIATVVALGSYFYTLHKRNKKK----MVELYOTEN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE005173; NID: g11067299; PIDN: AAG28826.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAFIA!FSFFMVKHKFTPF----TINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IWFSTFLETAGFPVIFIPLLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 LIFTAIFAAIINRFKFTRWIILSIIGSILIYVFGSPEFG--GEPD----ENEEFYSIQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVAAAVMYAFILPLVELAYOKA-KOTMSY-----TLVLEFQLILCLLASIVSVIGMFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        283 VLLPITEVLAVIFYHEKFQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                            320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%; Score 282; DB 2; L. 26.0%; Pred. No. 3.9e-14; ive 78; Mismatches 145;
                                                                                                   346 PIVSVLVVIFFNFMDDEFDAFKGVALVTAVLSAAAYFF
                                                            PITEVLAVIFYH---EKFQAEKGLSLALSLWGFVSYFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 CIILAIGNCGGPLIMRL -- YFNNGGKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 26.0°
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-390 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: T15M6.24
                                                   286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
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C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: G86330
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                          125 FFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFI 184
                                                                                                                                                                                                                                                                                                                                                                                  ::: | | ::|: |: | ::: | :: ::: | :: |:: | :: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 VIYVLTLVGTAVSMQLGSVGAVALIFLVSSLFSNLIGTLSLIVTPLAAIAVFHDKLTEVK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005172; NID:g10086493; PIDN:AAG12553.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 TAQLFFTPIFAAFINKIKFNRWVVISVILAIITGALTLSSSFGGEP-DEAEENYARGSWA 226
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                                                                                                                                                               NVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 ALFYVVAVFSAIIWQGPFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEK 304
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            64
LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSN
                                                        227 ALFAGICFALLLCNIQNVFDSYIFKRTESTNQKPSFASVFEVIIFSSLVATIISVVGLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 LPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: :: | | | :: | :: | :: | :: | WAMLIAFMGFGFYIY---QNYLDDLKVQRAREAQAE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVAAAVMYAFILPLVELAY-----
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-393 <STO>
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13

116

157

282

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225

Length 389;

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15.8%;
                    Query Match 15.8
Best Local Similarity 24.9
Matches 90; Conservative
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Best Local Similarity
Matches 85; Conserva
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A; Residues: 1-398 <S
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: 86516
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nathors: Hunter, J.L.; J. Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Alther: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Attle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                           Status: preliminary
!Molecule type: DMA
| Residues: 1-392 <STO>
| Gross-references: GB:AE005173; NID:95668799; PIDN:AAD46025.1; GSPDB:GN00141
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tive 74; Mismatches 153;
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Best Local Similarity
Matches 90; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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C, Genetics:
A, Gene: F16N3.10
A, Map position: 1
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; Score 277.5; DB 2;
; Pred. No. 8.4e-14;
68; Mismatches 151;
                                                                                                                                                                                                                                                                          10 CIILAIGNCGG-----PLIMRLYFNNGG-----
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200 PDFGGQPHDGEEFGYNIQAWLAFSATIAFSLSLCLIQLGFEKLQVKTKRYGNEKVFRMVL 259

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Search completed: September 23, 2004, 23:51:18 Job time : 26.8588 secs

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2004
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1/35 1 MKNGLIIINCIILTIGTCGG.......DKPQPPETELPILPVSDYVA 356 Perfect score: Sequence: Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
3: pir2:*
: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	purine permease (i	hypothetical prote					_	_				ρ	unknown protein Ti	F16N3.10 [imported	hypothetical_prote	hypothetical prote	44	related to UDP N-A	hypothetical prote	conserved hypothet				conserved hypothet	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	ы
SUMMARIES	ID	D86408	B84749	C86408	D96506	T04924	T04923	T04922	A84634	T04921	C85087	G86330	E96516	D96613	H96516	C96613	H86232	C69725	T50997	T10557	C69212	F83698	A96507	A83892	AE1193	F72219	D71181	G69766	A83049	S29685
	DB	7	~	7	~	7	7	~	~	~	~	~	~	~	~	~	~	N	N	N	7	N	~	7	~	~	~	~	N	~
	Length	356	356	351	379	344	348	1128	315	358	432	393	389	390	392	398	383	470	357	368	343	311	370	298	348	288	292	287	297	629
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hypothetical prote	conserved hypothet	hypothetical prote	chloramphenicol re	hypothetical prote	probable permease	nodulin-like prote	conserved hypothet	hypothetical 30.5K	sucrose uptake pro	conserved hypothet	unknown protein F1	probable transport	probable transport	hypothetical prote	
E71174	D75555	869718	C64923	E75159	C97242	H84792	AC1252	JS0384	JQ0781	AI1614	G96741	F90924	B85773	AB2471	T05133
8	0	~	٦	~	7	~	~	~	N	N	N	~	~	~	N
284	325	370	389	287	310	357	345	286	479	345	347	389	389	412	362
6.7	6.7	6.7	6.7	6.7	6.7	6.7	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.4
120.5	120.5	120.5	120.5	120	120	120	119.5	119	118	117.5	116.5	116.5	116.5	116	115.5
30	31	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 D86408 Oprine permease [imported] - Arabidopsis thal:	RESULT D86408 purine
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: Backer, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chacession: D86408
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Liu, X.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; D.; Yu, G.; Fraeer, C.M.; Venter, J.C.; Davis, R.W.
A,Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-356 <STC

A;Cross-references: GB:AE005172; NID:g9795614; PIDN:AAF98432.1; GSPDB:GN00141 C;Genetics: A;Map position: 1 C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70 <STO

ö 0; Gaps Length 356; Indels Score 1792; DB 2; Pred. No. 1.3e-135; 0; Mismatches 1; Query Match
Best Local Similarity 99.7%;
Matches 355; Conservative

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RRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG 120 61 RESNRNPUNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG 120 9 61 유 ò 셤

240 181 VVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAR 240 181 VVAALLYAFILPLVELTYKKARQEITFPLVLBIOMVMCLAATFFCVIGMFIVGDFKVIAR ð g

241 EAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVV 300 241 EAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVV 300 δ 요

CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPILPVSDYVA 356 301

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Gaps

11;

66; Indels

DB 2;

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RRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 BAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLFVTEVFAVV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-351 <STO>
A,Crosers references: GB:AE005172; NID:g9795615; PIDN:AAF98433.1; GSPDB:GN00141
C,Genetics:
A,Map position: 1
C,Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 FYHEKPQAEKGISLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSG--KKVVDKPQPPETELPIL--PVSD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                181 VVAALLYAFILPIVELTYKKARQEITFPLVLEIOMVMCLAATFFCVIGMFIVGDFKVIAR
                                                                                                                                                                                                                                                                                                                                                                                               1 MKNGLIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSR
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C86408
A;Status: preliminary
                                                                                                                                                                                                                                                                                 / Match 63.1%; Score 1134.5; DB 1. Local Similarity 59.9%; Pred. No. 3.7e-83; les 214; Conservative 66; Mismatched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <STO>
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A,Gene: T12C22.2
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Best Local Si
Matches 214;
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F3H9.12 protein - Arabidopsis thaliana (mouse-ear cress)

C;Species arabidopsis thaliana (mouse-ear cress)

C;Species arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001

S;Recession: C86408

C;Accession: C86408

K;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, D.

Anture 408, 816-820, 2000

A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Marziali, R.; Rowley, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
                                                                                                                                 Pypothetical protein At2933750 [imported] - Arabidopsis thaliana C; Species: Atabidopsis thaliana (mouse-ear cress)
C; Species: Atabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
R; Atal, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Accession: B84749
A; Accession: B84749
A; Accession: B84749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VVAALLYARTILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFK---- 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPVTEVFAVVCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPIL 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule rype: DNA
A;Residues: 1-356 <STO>
A;Cross-references: GB:AE002093; NID:g1707019; PIDN:AAC69140.1; GSPDB:GN00139
C;Genetics:
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                   CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPILPVSDYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: At2g33750
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
64.5%; Score 1160; DB 2; Length 356;
Best Local Similarity 62.9%; Pred. No. 3.5e-85;
Matches 231; Conservative 45; Mismatches 69; Indels 2:
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hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana hypothetical protein T12C22.2 [imported] - Arabidopsis thaliana (mouse-ear cress) (c.Species: Arabidopsis thaliana (mouse-ear cress) (c.Species: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C.Accession: D96506 (c.M.) c.M.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Theologis, A.; Ecker, J.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature, J.L.; Jonkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., A.; Li, J.H.; Y.; Liu, X.; Liu, Z.A.; Luvos, J.S.; Maiti, R.; Marziali, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luvos, J.S.; Maiti, R.; Marziali, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.A.; Talles Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB;AE005173; NID:g8655985; PIDN:AAF78258.1; GSPDB:GN00141
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30.6%; Score 550; DB 2; Length 379;
Best Local Similarity 34.4%; Pred. No. 1.7e-36;
Matches 119; Conservative 74; Mismatches 133; Indels 20;
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C; Accession: T0493-3
R; Bevan, M.; Murphy, G; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, February 1999
A; Reference number: Z15390
A; Accession: T04923
A; Molecula control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 KFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVEL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 KLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQ 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYAL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 TNGG----SGVYYDNGGNSKWLATVVQLVGFPVILLPYYILSFKTHATTDRDGKRTSPRNRV 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 IVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKTKLFLMETPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: T9A21.60
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
30.2%; Score 543; DB 2; Length 346
Best Local Similarity 34.4%; Pred. No. 5.7e-36;
Matches 116; Conservative 69; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-348 <BEV>
A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar Columbia; BAC clone T9A21
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: cultivar Columbia, BAC clone T9A21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 29.7%; Score 533.5; DB 2; Best Local Similarity 34.8%; Pred. No. 1e-34; Matches 114; Conservative 72; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>::</u>
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A; Introns: 76/2; 402/1; 526/3; 762/1
A; Note: T9A21.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1128 <BEV>
A;Cross-references: EMBL:AL021713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T04924
R; Beyan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, February 1999
A; Reference number: Z15390
A; Accession: T04924
A; Molecule type: DNA
A; Residues: 1-344 <BEV>
                                                                                                                                                                                                                                                                                      214 ALYSLLLSLMQFSFEKILKRETFSVVLEMQIYTSLVATCVSVIGLFASGEWRTLHGEMEG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 YH-KGQASYVLILVWTAVTWQVCSVGVVGLIFLVTSLFSNVISTLSLAVTFLAALVVFRD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNALFAFLLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAA 184
                                                                                                                                                                                                                                                                                                                                                                                                 LLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREARE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 NKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLA 124
                                                                                                                                                                       ASVESSESSCSLKY----IVLIYVLLGVIIAGDNMLYSVGLLYLSASTYSLICATQLA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEXVVGFLMTVVAALLYAFIL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 FYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYVMNLVWTAVTWQVFSIGCTGLIFELSSLFSNAISALGLPVVPILAVIIFHDKMNGLKV 295
                   LVSVNIFFLIGGQAASVLLGRFYYDEGGNSKWMATLVQTAAFPILYIPLLL----LPSS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T9A21.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAE
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A,Introns: 11/1
A,Note: T9A21.70
C,Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 KFQAEKGVSLLLSLWGFVSYFYGEFKSGKKV------VDKPQPP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
30.3%; Score 545.5; DB 2; Length
Best Local Similarity 35.1%; Pred. No. 3.6e-36;
Matches 120; Conservative 69; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 VSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPILPVSD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar Columbia; BAC clone T9A21
                                                                                                                                                                                                                                                                                                                          154
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hypothetical protein AT4g08700 [imported] - Arabidopsis thaliana hypothetical protein AT4g08700 [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C;Accession: C85087

A;Attle: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; MUID:20083488; PMID:10617198

A;Accession: C85087

A;Accession: C85087

A;Molecule type: DNA

A;Residues: 1-432 <STO>
                                                  C;Species: Arabidopsis thaliana mouse-car cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C;Accession: T04921
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X. submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKES----KKEYVVGFLMTVVAAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYFLNSQKITPFILNSLVLLTISSTLLVIQHEPESPSSTŠKSAAKSKYVIGYICAVGSSA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 KIGGSVFYYALIVI-TGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 ILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --NKRKĮKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 LYAFILPLVELTYKKARQEITFPLVLEIOMVMCLAATFFCVIGMFIVGDFKVIAREAREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 LILAGETIATLIGRLYYEKGGKSTW----LET----LVQLP-----EPSKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 358;
                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 EMSGIKLVAMFLAIWGFVSYGYQHYVNDRKPEEDQELPQSK 343
                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-358 <BEV>
A;Cross-references: EMBL:AL021713
A;Experimental source: cultivar Columbia; BAC clone T9A21
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.3%; Score 473.5; DB 2; 32.6%; Pred. No. 2.5e-30; ive 73; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 494.5; DB 2;
Pred. No. 4.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.5%; Score 494.5; DB 2; Best Local Similarity 34.6%; Pred. No. 4.46-32; Matches 118; Conservative 71; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 26.3
Best Local Similarity 32.6
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 60/3
A;Note: T9A21.30
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hypothetical protein At2g24220 [imported] - Arabidopsis thaliana
hypothetical protein At2g24220 [imported] - Arabidopsis thaliana
C;Species Arabidopsis thaliana (mouse-ear cress)
C;Species Arabidopsis thaliania (mouse-ear cress)
C;Species A84634
R;Lin, X:, Kaul, S:, Rounsley, S.D.; Short, D. Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K;Lin, X:, Kaul, S.; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLWGF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
                                                                                                                                           GFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLWGFVSYF 325
                                                                                                                                                                                                                                                                                                         308 VYTIGVVGLIFESSSVFSNSITAVGLPIVPVVAVIVFHDKANASKIFSIILAIWGFISFV 367
                                                             265
                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: GB:AE002093; NID:g4115382; PIDN:AAD03383.1; GSPDB:GN00139
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 ETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFILVKQKFTPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 SINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKTKLFLM
                                                                                                                                                                                                 TPPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQ
77 VYYENGGKSTWMGTLVQLIGFPVL---FLFRFFSQTK-NPKPTEADFRK----FSSFTIL
                                     FIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINA
                                                                                                                   146 VVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQEI
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29.6%; Score 531.5; DB 2; Length 315;
Best Local Similarity 36.8%; Pred. No. 4.3e-35;
Matches 114; Conservative 67; Mismatches 114; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: At2g24220
A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70
                                                                                                                                                                                                                                                                                                                                                                                                       368 YQHYLDEKKLKTSHTSPVGDPHLLPAEE 395
                                                                                                                                                                                                                                                                                                                                                                    YGEFKSGKKVVDKPQPPETELPILPVSD 353
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Matches
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Nature 408, 816-820, 2009
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status; preliminary
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                                                                                                                                                             A;Cross-references: GB:AE005172; NID:g10086493; PIDN:AAG12553.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHSSSSSCFKTLVWIY-----LSLGFAIGLDNLLYSFGLLYLSASTYSILCSSQLA 136
                                                                                                                                         FNALFAFLLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAA 184
                                                                                                                                                                                                              LLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREARE 244
                                                                                                                                                                                                                                                                                    FKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 SFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLIIGTQLAFNALPAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFLMTVVAALLYAFILPLVELTY-----KKARQEITFPLVLEIQMVMCLAATFFCVI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSWAALFAGICFALLLCNIQNVFDSYIFKRTESTNÖKPSFASVFEVIIFSSLVÄTIISVV 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMFIVGDFKVIAREAREFKIG-GSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVL 286
                                                                  RNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
LIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F6F9.18 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                           KFQAEKGVSLLLSLWGFVSYFYGEFKSGKKV 335
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Best Local Similarity
Matches 93; Conserv
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A; Residues: 1-393 <STO>
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Chin, C.W.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C., L.; J.H.; Y.; Lin, X.; Liu, Z.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96613
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
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A;Authors: Hunner, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
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                                                                                                                                                                                                                                                               F16N3.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: E96516
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287 ISVLLPVTEVFAVVCFR---EKFQAEKGVSLLLSLWGFVSYFYGEFKSGK 333
                                            341 SVITWPIVSVLVVIFFNFMDDEFDAFKGVALVTAVLSAAAYFFRLHKDNR 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 389;
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60; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 313; DB 2; 28.0%; Pred. No. 1.4e-17;
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es 98; Conserva
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A;Status: preliminary
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207 223

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hypothecical protein F13D13.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: C96613
R;Theologis, A.; Eck.
C;A. Ccession: C96613
R;Theologis, A.; Eck.
C;A. Cin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
A;Authors: All Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
A;Ritle: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Accession: C96613
A;Scatus: preliminary
A;Accession: C96613
A;Accession: C96613
A;Accession: C96613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE005173; NID: 911128382; PIDN: AAG31188.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 KGTWIQALIQNAAFP-ILIPLFFIF------PKPKQHLETNNISFLSLRLFFLYLSL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHSDGDK--P 165
                                                                                                                                                                                                                                                                                                                                                224 FCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLAS 283
                                     48 IFVCSCLVVA-GRVLSTLLINFYFIQTGRDVCDDPKQFKGTWLQSMVQNAAFPFTAFLLL 106
                                                                                                    55 V---SFLSRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYG----L 107
                                                                                                                                                     107 LWRSSF-----STHSETSSSSSF---GKLFLLYISLGVLFAAYSQLYAIGRTHCV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 GLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 TEPLVLBIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 IGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKAR------QEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 KRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKTKLFLMETPLFIASIVI
                                                                                                                                                                                                                                         166 AKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKA--RQEITFPLVLEIQMVMCLAATF
5 LIIINCIILTIGTCGGPLLTRLYFTNGGKRI------WFMSFLSTAGFPIILIPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 GVLISVLLPVTEVFAVVCFR----EKFQAEKGVSLLLSLWGFVSYFYGEFKSGKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Score 271; DB 2; Length 398; 25.2%; Pred. No. 3.3e-14; rive 65; Mismatches 157; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-398 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
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Best Local S:
Matches 82
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F16M3.10 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: H96516
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudpes, B.; Hudzer, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.A.; Liu, Z.A.; Lincos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Atthele Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Reference trype: DNA
A;Residues: preliminary
A;Molecule trype: DNA
A;Residues: 1-392 (2702)
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFLMTVVAALLYAAFILPLVELTYKKA-----RQEITFPLVLEIQMVMCLAATFFCVIG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MFIVGDFKVIAREAREFKIGGSVFYYALIVI-TGIIWQGFFLGAIGIVFCASSLASGVLI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 LFASGENKELGGDSHRFKKGET--YYVLSLIGLALSWQVWAVGLMGLVLYVSGVFGDVVH 326
                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-390 <STO>
A;Residues: 1-390 <STO>
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C;Genetics:
A;Gene: T15M6.24
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 IGTQLAFNALFAFLLVKQKFTPFSINAVVLLTVG---IGILALHSDGDKPAKESKKEYVV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRRRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLI 118
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIILT-IGTCGGPLLTRLYFTNGGKR-----IWFMSFLSTAGFPIILIPLLVSFL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 CIFLVLLGDSLVMLLLNFFYVQDNREDSDQDLQYRGTWLQALVQNAAFP-LLIPLFFFF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 SVLLPVTEVFAVVCF---REKFQAEKGVSLLLSLWGFVSYFYGEFKSGKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                   16.0%; Score 287; DB 2; Length 39 25.4%; Pred. No. 1.7e-15; ive 71; Mismatches 148; Indels
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15.7%; Score 282.5; DB 2;
Best Local Similarity 26.4%; Pred. No. 3.9e-15;
Matches 94; Conservative 65; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.4%
Matches 89; Conservative
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265

313 VWAVGMIGLVHYVSGLFGDVVHMCASPFVALFVVLAFDFMDDVFSWPRIGALIGTVLALG 372

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Search completed: September 23, 2004, 23:51:16 Job time: 27.1412 secs

THIS PAGE OF WAY WEEK.

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September 23, 2004, 23:50:27; Search time 85.017 Seconds (without alignments) 1331.366 Million cell updates/sec
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1 MVKALVIINCIILAIGNCGG......QQEESQETEQSSLSRPISEC 352
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1349238 segs, 321558718 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	173116,	160022,	216343,	44529, A	184544,	193908,	245361,	239885,	45366,	146343,	61519, A	174206,	70607, A	174205,	136993,
c		• •				•			_			• • •	-	•	• •
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES ID	US-10-424-599-173116	US-10-437-963-160022	US-10-424-599-216343	US-10-425-114-44529	US-10-437-963-184544	US-10-437-963-193908	US-10-424-599-245361	US-10-424-599-239885	US-10-424-599-145366	US-10-437-963-146343	US-10-425-114-61519	US-10-424-599-174206	US-10-425-114-70607	US-10-424-599-174205	US-10-437-963-136993
	12	91	12	12	16	. 91	12	12	77	. 91	12	77	77	12	16
* Query Match Length DB	320	390	306	293	423	391	362	409	366	751	267	355	246	363	372
\$ Query Match	51.6	49.2	47.8	47.2	35.2	33.6	32.5	31.4	30.7	30.3	30.0	28.9	28.4	28.1	28.0
Score	606	998	841.5	830	619.5	590.5	572.5	552.5	540	534	528	508.5	500.5	494.5	492
Result No.	-	7	ю	4	S	9	7	80	σ	10	11	12	13	14	15

16	489.5	27.8	216	16	US-10-437-963-174935	Sequence 174935,	
17	489.5	27.8	379	12	US-10-425-114-45872	Sequence 45872, A	
18	476.5	27.1	400	16	US-10-437-963-104380		
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20	472.5	26.8	610	16	US-10-437-963-186383	Sequence 186383,	
21	471	26.8	379	16	US-10-437-963-121341	Sequence 121341,	
22	441.5	25.1	327	12	US-10-424-599-218003		
23	407.5	23.2	238	12	US-10-424-599-204152	Sequence 204152,	
24	343	19.5	241	12	US-10-424-599-152055		
25	294	16.7	202	16	10-767-		
56	270.5	15.4	164	16	US-10-767-701-40564	Sequence 40564, A	
27	235.5	13.4	166	16	US-10-767-701-35609		
28	228.5	13.0	173	12	US-10-424-599-257773		
53	216.5	12.3	70	12	US-10-424-599-261293		
30	202	11.5	167	16	US-10-767-701-35590	Sequence 35590, A	
31	194.5	11.1	150	16	US-10-767-701-37550		
32	167.5	9.5	94	12	US-10-424-599-263994	Sequence 263994,	
33	156.5	6.8	357	16	US-10-437-963-151972		
34	138.5	7.9	358	16	US-10-437-963-186107		
35	136.5	7.8	388	12	US-10-425-114-44759	Sequence 44759, A	
36	134.5	7.6	296	19	US-10-767-701-35041		
37	133.5	7.6	314	12	US-10-282-122A-53153		
38	132	7.5	102	12	US-10-424-599-217019	21701	
39	131	7.4	327	12	US-10-424-599-271242		
40	130.5	7.4	380	16	US-10-437-963-106742	10674	
41	129.5	7.4	369	12	US-10-425-114-64886	_	
42	129.5	7.4	265	16	US-10-437-963-147143	Sequence 147143,	
43	129	7.3	596	0	US-09-815-242-5098	Sequence 5098, Ap	
44	129	7.3	296	12	US-10-282-122A-43609	Sequence 43609, A	
. 45	128.5	7.3	313	17	US-10-425-114-72516	Sequence 72516, A	

ALIGNMENTS

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US-10-424-599-173116

Sequence 173116, Application US/10424599

Sequence 173116, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: Rowalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 173116

LENGTH: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ALIGLITGLDDYLYACGVARLPVSTFSLIQASHLAFTAVFAFLLVRHRFTPYSVNSLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAFILPLVELAYQKAKQTMSYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.6%; Score 909; DB 12; Length 320; 55.2%; Pred. No. 3.7e-81; ive 66; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_12733C.1.pep
US-10-424-599-173116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.2%
Matches 170; Conservative
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Sequence 44529, Application US/10425114

| Bublication No. US20040034888A1
| Publication No. US20040034888A1
| Bublication No. US2004003488BA1
| APPLICANT: Liu, Jingdong
| APPLICANT: Liu, Jingdong
| APPLICANT: Accept, Steven E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Pabaska, Jack E
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| APPLICANT: Pabaska,
                      GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Sou Vihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

ERO ID NO 216343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 VMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAR 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
47.8%; Score 841.5; DB 12; Length
Best Local Similarity 54.6%; Pred. No. 1.6e-74;
Matches 160; Conservative 59; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_37387C.1.pep
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; OTHER INFORMATION: Clone ID: 700941791_FLI.pep
US-10-425-114-44529
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (1)..(306)
OTHER INFORMATION: unsure at all Xaa locations
Publication No. US20040031072A1
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ORGANISM: Glycine max
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 PKBAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAV 293
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                               VLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFL
                                                            GAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLALSLWGFVSYFYGEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_59340C.1.pep
US-10-437-963-160022
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MFFHEPFNGTKGVALALSLWGFVSYFYGEVRAAKAAHR 375
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al Similarity 47.6%; Pred. No. 8.4e-77;
161; Conservative 85; Mismatches 80;
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US-10-424-599-216343
; Sequence 216343, Application US/10424599
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 160022, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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                                                                                                                                                                                                                                                           324 KSGEDKRR 331
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KQDREKNK 304
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Best Local Similarity
Matches 161; Conserv
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US-10-437-963-160022
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LENGTH: 390
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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APPLICANT: Li, Fing
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 193908
LENGTH: 391
                                                           328 LSYVMTLLWTAISWQVASVGVVGLIFVVSSLFSNVISTLALDIIPVFAVIPFHDXMDGVK 387
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245 ALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQAEK 304
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US-10-437-963-193908
                                                                                                                                                                                       305 GLSLALSLWGFVSY---FYGEIKSGEDKRRIQQEES 337
                                                                                                                                                                                                                                             388 IIAMLMAIWGFMSYGHQLYVDGKKGR-KTTVSVEET 422
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OTHER INFORMATION: unsure at all Xaa locations
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US-10-424-599-245361
; Sequence 245361, Application US/10424599
; Publication No. US20040031072A1
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBNCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 184544
                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                LIIASQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 FLITVAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:::||| :| ||:|||:|| |:|::|:||:||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:||
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                                                                                                                                                                                                                         51 IPLLFSYITRRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAA
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                                  Length 293;
                                                                                                                                     60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 LAVIVYKESFHAEKGVALVLSLWGFVSYFYGEIKQDREKNK 277
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US-10-437-963-184544
                                  ; Score 830; DB 12;
; Pred. No. 2.1e-73;
63; Mismatches 60;
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Publication No. US20040123343A1
GENERAL INFORMATION:
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Barbazuk, Brad
                                       47.2%;
54.8%;
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APPLICANT: Kovalic, David K.
APPLICANT: Ebou, Yihua
APPLICANT: Cao, Yongwei
                             Query Match
Best Local Similarity 54.8
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-437-963-184544
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APPLICANT:
APPLICANT:
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APPLICANT: La Novalic David K
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1912313 B
FILE REPREMENT 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 145366
LENGTH: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 KPRLLIAAVI-----VGILSGFDNYLYAYGIAYLFVSTAALIIASQLAFIAIFSFFMVK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 HKFTPFTINAVVLLTVGAAVLGMHTETDKPVHE-----THKQYITGFLITVAAAVMYA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 LKFTPYIINSLVLTISSTLLVFQNESSSDDDDDSDSTKISKKKXVIGFICTVGASAGYG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 KGSRVYWVTVMGNVVTWQLCFMGTAGMVFLTSSLTGGICMTFLLSMNVLGGVVFFRDAFG 354
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                                                                                                                                                                                                                                                                                                            62 RSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIA 121
                                                                                                                                                                                                                                                                                                                                      126 VPFN--DFT-----PRMLIISISIGVMLGFNNLFPSWGNSYLPVSTSALLLSSQLLFNL 177
                                                                                                                                                                                                                                                                                                                                                                                                   122 IRSFFWYKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMY 181
                                                                                                                                                                                                                                                                                                                                                                                                                               242 LGBALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 CGSAAİLLGRLYYEKGGKSKWMGTLVQLAGFP---İQLPFHFİS--ASKNLTINSS---İ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 CGGPLIM--RLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRRSNNVGDSTSFFLI
                                                                                                                                                                                                                        5 LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYI---TRR
                                                                                                                                                                                 Indels 17;
                                                                                                                                    DB 12; Length 409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.7%; Score 540; DB 12; Length 36
34.8%; Pred. No. 1.2e-44;
ive 80; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_102285C.1.pep
US-10-424-599-145366
LOCATION: (1)..(409)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
CHER INFORMATION: Clone ID: PAT_MRT3847_58641C.1.pep
US-10-424-599-239885
                                                                                                                                       Query Match 31.4%; Score 552.5; DB 12; Best Local Similarity 34.1%; Pred. No. 8.2e.46; Matches 118; Conservative 79; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145366, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Best Local Similarity 34.8
Matches 123; Conservative
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ORGANISM: Glycine max
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US-10-424-599-145366
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REFERENCE: 38-21(53223) B

CURRENT APPLICANT: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

EBNGTH: 409
                                  APPLICANT: LESSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Anou Yihua
APPLICANT: Show Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 362
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90 SASPP----IKIILLIXXVF-GVLIAADNMMYSTGLLYLSASTYSLICASQLAFNAVFS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 VAYVMILVWTSIAWQVCSVGVVGLIFLVSSLYSNVISTVSLAVTPIAAVIVFHDKANGVK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 FFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMXAFI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 NVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIALFS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || :: | :| |: || || 30 LVTLSIAFLIVGSAAVILGREYYDQGGNSKMWATLVQTAARPILFIPLFTIPSPPEAST 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 LSLMQLTFEKVLKKETFSVVLEMQIYTSFVASGASVIGLFASGEWR-TLHGEMEGFQKGY
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32.5%; Score 572.5; DB 12; Length 362;
Best Local Similarity 36.3%; Pred. No. 7.4e-48;
Matches 123; Conservative 72; Mismatches 137; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 GLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_63592C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(362)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Glycine max
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NAME/KEY: unsure
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NAME/KEY: unsure
LOCATION: (1)..(3
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Sequence 174206, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Roba Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 174206

LENGTH: 355
                                                                                                                                                                                                                Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AIFSFFWYGHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQY1TGFLITVAAAVM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 MRRILVATNCVMLALGVTGGQLLSRLYFSKGGHRQWLSGWLQTGGWDLLLPPVAASYV-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 YAFILPLVELAYQKAK---QTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zho, Tinguana APPLICANT: Zho, Tinguana APPLICANT: Zho, Yihua APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asscritte OF INVENTION: Nucleic Acid Molecules and Other Molecules Asscritte OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPRENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61519
LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72; Indels
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US-10-424-599-174206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-024-D8_FLI.pep
US-10-425-114-61519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
30.0%; Score 528; DB 12;
Best Local Similarity 43.8%; Pred. No. 1.2e-43;
Matches 102; Conservative 55; Mismatches 72;
Publication No. US20040034888A1
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Best Local Similarity 32.2<sup>3</sup>
Matches 104; Conservative
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US-10-424-599-174206
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                               200 LWLSLTQLVFKKVIKRETFKVVLDMILYTSLVATLATLVGLFASGEW-SGLKNEMKEYEL 258
                                                                                                                                                      243 GEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 KSPSSCTNTPWAK--LAVIXIVLGLIIAADDMMYTGGLKYLPASTYSLICASQLAFNVVF 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 NNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAF 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITRRS
                   183 FILPLVELAYOKAKOTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKL
                                                                                                                                                                                                                            303 EKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSS----LSRPISE 351
                                                                                                                                                                                                                                                                16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT4530_46977C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.3%; Score 534; DB 16; 30.9%; Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 146343, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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US-10-425-114-61519
; Sequence 61519, Application US/10425114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Matches 108; Conservative
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ORGANISM: Oryza sativa
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Query Match
Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 GGRSAYYLVIIWGAITFQLGVLGGTAVIFLGSTVLAGVLNAVRTPITSIAAVILLKDFMS 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                   122 IFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMY 181
                                                                                                                     182 AFILPLVELAYOKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFK 241
                                                                                                                                                                                242 LGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQ 301
62 RSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVKALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLLFSYITR
                                                                                                                                        211 GLIFALSELVFVKLLERRSFIVVLEQQVMVSLFAFLFTTVGMIMSGDF-QGMAHEATTFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Clone ID: LIB3608-022-E3_FLI.pep
US-10-425-114-70607
                                                                                                                                                                                                                                                                                                                         RESULT 13
US-10-425-114-70607
Sequence 70607, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
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US-10-424-599-174205
; Sequence 174205, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                 302 AEKGLSLALSLWGFVSYFYGEIK 324
                                                                                                                                                                                                                                                                    181 YAFILPLVELAYOKA 195
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YGLVLPLVELAYRRA 243
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ORGANISM: Zea mays
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| Sequence 136993, Application US/10437963
| Sequence 136993, Application US/10437963
| Publication No. US20040123343A1
| Publication No. US20040123343A1
| GENERAL INFORMATION:
| APPLICANT: La Royalic, David K. APPLICANT: Zhou, Yihuav J. APPLICANT: Cao, Yongwei J. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad J. APPLICANT: His Ping J. APPLICANT: Li, Ping J. TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement J. TILE OF INVENTION: Plants and Uses J. (51221) B. CURRENT APPLICATION NUMBER: US/10/437,963
| CURRENT PLING DATE: 2003-05-14
| SEQ ID NO 136993 | LENGTH: 372
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zoo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 14205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GGRSAYYLVIIWGAITFQLGVLGGTAIIFLGSTVLAGVLNAVRTPITSIAAVILKDPMS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 LGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLLPITEVLAVIFYHEKFQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 IFSFFWVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAAAVMY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 AFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 GLIFALSELVFVKLLGRRSFIVVLEQQVWVSLFAFLFTFVGMIVSGDF-QGMAHEATTFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFP----VIFIPLLFSYITRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.1%; Score 494.5; DB 12; Length : 31.6%; Pred. No. 3.7e-40; tive 81; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_128326C.1.pep
US-10-424-599-174205
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(363)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
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Query Match 28.0%; Score 492; DB 16; Length 372; Best Local Similarity 30.7%; Pred. No. 6.8e-40; Matches 102; Conservative 81; Mismatches 115; Indels 34; Gaps
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38519C.1.pep
US-10-437-963-136993
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3 KALVIINCIILAIGNCGGPLIMRLYFNNGGKRIWFSTFLETAGFPVIFIPLL 54 	55FSYITRRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLYAYGIAYLFVSTAALI 112 	113 IASQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITG 170 	I FLITVAAAVMYAFILPLVELAYQKAKQTMSYTLVLEFQLILCLLASIVSVIGMFIAGDFK 230 	231 QALPKEAREFKLGEALFYVVAVFSAIIWGFFLGAIGLIFSTSSLVSGIMISVLLPITEV 290 	291 LAVIFYHEKFQAEKGLSLALSIWGFVSYFYGE 322
3 KJ : 19 RI	55 79 RI	113 IX	171 FI 182 F2	231 QA : 241 EE	291 LJ 297 GC
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September 23, 2004, 23:40:51; Search time 14.9153 Seconds (without alignments) 1228.856 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-913-767-9
1760
1 MVKALVIINCIILAIGNCGG......QQEESQETEQSSLSRPISEC 352

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P07869 bacillus su Q05394 oryccolagus Q09191 salmonella P94486 bacillus su Q01345 oncorhynchu P48761 cricetulus Q56072 salmonella P42394 buchnera ap Q01650 homo sapien Q92127 mus musculu P33031 escherichia Q9ux84 sulfolobus
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# ALIGNMENTS

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                                                                                                                  PRT;
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Soehling B., Gottschalk G.;
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                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33507 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, L21902, AAA92345.1; -.
Interpro, IPR000620; DUF6.
Pfam, PF00892; DUF6; 2.
Hypothetical protein; Transpo
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=1534;
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ID YCAY CLOKL
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                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 KNILVMSLTITGVLSLİFTPLFLFFRAPVMAETMLTDKRTLYPLLAITPVVPIIAİSSVLR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YLYAYGIAYLPVSTAALIIASQLAFIAI 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 FSFFMVKHKFT-------PFT-INAVVLLTVGAAVLGMHTETDKPVHETH- 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------KQY--ITGF---LITVAAAVMYAFILPLV----ELAYQKAKQTMSYTL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 VLEFQLILCLLASIVSVIGMFIAGDFKQALPKEAREFKLGEA--------LFYV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 VAVFSAII------WQGFFLGAI---GLIFSTSSLVS-GIMISVLLPITEVLAVIFY 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | | : : | | | : : | 201 YLFYCEKYKKTIKIRKHFLQSIKNGKQTFTQLMSVSLPTTGSRFIGNLSWFFBPIVVAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 KRIWFSTFLETAGFPVIFIPLLFSYITRRSNNVGDSTSFF-----LIKPRLLIAAVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Mismatches 137; Indels 117; Gaps
      Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subcilis.";
                                                              FUNCTION: SPOYS PROTEIN IS INVOLVED, DIRECTLY OR INDIRECTLY, IN SPORE CORTEX BIOSYNTHESIS AND AFFECTS ONLY INDIRECTLY EXPRESSION OF LATE SPORULATION GENES.

SUBCELLULAR LOCATION: Integral membrane protein (Probable).

BUBCILOPMENTAL STAGE: SPONY TRANSCRIPTION TAKES PLACE DURING THE SECOND HOUR OF SPORULATION. IT MAY BE TRANSCRIBED MAINLY, IF NOT ONLY, IN THE MOTHER CELL. INDEED, IT IS REQUIRED ONLY IN THE MOTHER CELL.
                                                                                                                                                                         SIMILARITY: Belongs to the polysaccharide synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 134; DB 1; Length 518;
21.7%; Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF01943, Polybacc_synt, 1.
Sporulation, Transmembrane, Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                      SubtiList; BG10778; spoVB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Conservative
                                                           Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YTVISKKRIEIYGGYVFN 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 IILLEPMAVKDIKVKKLKLTGNDLGYL-----ALCGILAVSISMRQFAVTYTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVHETHKQYITGFLITVAAAVMYAFILPELVELAYQKAKQTMSYTLVLE-----FQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular analysis of the anaerobic succinate degradation pathway
                                                                                                                                                                                                                                                                                                                           Clostridium kluyveri.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium kluyveri.";
J. Bacteriol. 178:871-880(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 311;
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tive 62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the eamA transporter family.
                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical transport protein in catl 5'region (ORFY).
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297 HEKFQA-----EKGLSLA-LSLWGFVS 317
                                                                                                                                                                                     311 AA
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432 HAATVSKVLPISIKIKEYALSFAVIVICGFIS
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                                                                                          147 AAVLGMHT------ETDKPVHETHKQ----YITGFLITVAAAVMYAF--ILPLVEL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98037514; PubMed-9371463;

MEDLINE-98037514; PubMed-9371463;

Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K.,

Harrison D., Hoang L., Kagle P., Lumm W., Pothier B., Qiu D.,

Spadafora R., Vicare K., Wang Y., Wierzbowski J., Gibson R.,

Janai N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

-I. SUBCELLULAR LOCATION: Integral membrane protein (Probable).
                                 382 FSLYGYITTNKEYKDLLDKANSPIQVISOLKGYPYÍNPLLSLSLAITIFSFVGIPÞLVGF
                                                                      191 AYQKAKQTMSYTLVLEFQLILCLLASIVSVIG-MFIAGDFKQA---LPKEAREFKLGEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Transmembrane; Complete proteome
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                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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                                                                                                                                         247 FYVVAVFSAIIWQGFFLGAIGLIFSTSSLVSGIMISVLL 285
                                                                                                                                                                      499 FKKGLIFEA----GDFKGRITLISSPFSITISIITLVIL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%; Score 121.5; DB 1;
23.1%; Pred. No. 0.12;
ive 50; Mismatches 126;
                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hypothetical transport protein MTH841.
                                                                                                                                                                                                                                                                   343 AA.
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15-JUL-1999 (Rel. 38, Last seqn
28-FEB-2003 (Rel. 41, Last ann
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InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
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                                                                                                                                                                                                                                                                   STANDARD;
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168
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Best Local Similarity
68; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Y841 METTH
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              IF-----STSSLVSGIMISVLLPITEVLAVIFYHEKFQAEKGLSLALSLWGFVSYFYGE 322
                                 235 ICYLGAIKETSAVTASTVFLIKPALATVLAILILGESIEVNVVIGIVFIIIGSI-INYSS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 YLYAYGIAYLPVSTAALI-----IASQLAFIAIFSFFWVKHKFTPFTINAVVLLTVG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STFLETAGFPVIFIPLLFSYITRRRSNNVGDSTSFFLIKPRLLIA---AVIVGILSGFDN 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90291512; PubMed=2357736;
Cummings D.J., McNally K.L., Domenico J.M., Matsuura E.T.;
"The complete DNA sequence of the mitochondrial genome of Podospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curr. Genet. 17:375-402(1990).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane.
CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cummings D.J., Domenico J.M.;
"Sequence analysis of mitochondrial DNA from Podospora anseri
Pervasiveness of a class I intron in three separate genes.";
J. Mol. Biol. 204:815-839(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 125.5; DB 1; Length 5 Best Local Similarity 24.7%; Pred. No. 0.099; Matches 69; Conservative 51; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the complex I subunit 2 family.
                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
NADH-ubiquinone oxidoxeductase chain 2 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00361; oxidored q1; 1. Oxidoreductase; NAD; UbIquinone; Mitochondrion; SEQUENCE 556 AA; 62554 MW; 5613ACB0D2324BAF
                                                                                                                                                                                                            PRT;
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MEDLINE=89125610; PubMed=2975708;
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InterPro; IPR001750; Oxidored_q1.
                                                                                 323 IKSGEDKRRIQQEESQET 340
                                                                                                       294 NKKANDLKKVANTSSAES 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X55026; CAA38765.1; -. EMBL; X14485; CAA32646.1; -.
                                                                                                                                                                                                            STANDARD;
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P15578;
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RA Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Chilling Worth T., Churcher C.M., RA Brooks K., Brown D., Brown D., Davis P., Fellwell T., Fraser A., R. Alorisoy S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., RA Holfroyd S., Mones M., Leather S., McDonald S., McLean J., RA Almes K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Almes K., Jones L., Jones M., Lackler S., Roben J., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens S., Stevens S., Skelton J., Simmonds M., Squares R., Squares S., Stevens S., Whitehead S., RA Taylor K., Taylor R.G., Tivey A., Rabben J., Gyrmonprez B., Wolcksert G., Aert R., Robben J., Gyrmonprez B., Weltjens I., Vonstreels E., Rieger M., Schaefer M., Meilbert H., Reinhardt R., Pohl T.M., Rager P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Rager P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Rager P., Zimmermann W., Wedler H., Reinhardt R., Hurst S.M., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Roberttti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Rather Stander M., Reinhardt R., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Rabbakovski G.V., Wasery D., Barrell B.G., Nurse P., R. Rhennes equence of Schizosaccharomyces pombe. ", Lather H. Rutter 415:871-880(2002).
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                                                 84 AGIFLFFIRETPLREHVLNAINRKGESEARIKRNDYLI---LLLTALLSTVIAPL---LF 137
                                                                                                                                                                                                            AGFPVIFI----PL---LFSYITRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFDNYLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDB1 SCHFO STANDARD; PRT, 374 AA. 010354, QURXS; QURXS; Created) 16-OCT-1996 (Rel. 34, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) Hypothetical protein C22812.01 in chromosome I. SPAC22E12.01 OR SPAC890.09.
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47 ITRVVIIVLIVLAMYFFSLLLSMMNKWIFSESKMDFQFFPLFLSSC---QMLVQMGFAKLT 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 MASSVLSGLRWALTQXLLLDHPWTSNPFTSLFALTPLMFLFLL-----VAGLIFEGPVRF
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=2043337; PubMed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VKALVIINCIILA--IGNCGGPLIMRLYFNNGGKRIWPSTFLETAGFPVIFIPLLFSYIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 120; DB 1; Length 374; 23.1%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                              349 POTENTIAL.
42300 MW; AES04D822FAF8B12 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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or send an email to license@isb-sib.ch)
                                                EMBL; Z70443; CAA9388 1; -.
PIR; T50265; T50365.
GeneDB SPombe; SPAC22E12.01; -.
GO; GO:0016810; C:membrane; ISS.
GO; GO:0006810; P:transport; ISS.
Hypothetical protein; Transmembrane.
TRANSMEM 50 70
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                                           EMBL; AL133498; CAB63500.1; -.
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GNUT OR PA2322.
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238
273
329
374 AA;
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Q9ZIJ1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---IMRLYFUNGGKRIWFSTFLET--AGFPVIF----
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.";
Nature 406:959-964(2000)."
                                                                                            PATHWAY: Gluconate utilization.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                Pfam; PF02447; GntP permease; 1.
TIGRFAMs; TIGR00791; gntP; 1.
Gluconate utilization; Sugar transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 450;
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                                                                                                                                          SIMILARITY: BELONGS TO THE GNTP FAMILY OF PERMEASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           403 SHVNDAGFWLVKQYFNMSVSETFKTWTAMETILSVVGLV 441
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Conservative 52; Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Zevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brington J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Britz C., Fujita M., Pujita Y., Fuhre S., Galizzi A., Galleron N.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.;

RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Haicch J., Harwood C.R., Henaut A.,

RA Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Breescan E., Pulic P., Purnelle B., Rapoport G., Rey M., Sadaie Y.,

RA Bacto T., Scanlan E., Schleich S., Schroceter R., Scoffone F.,

Sekiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Takeuchi M., Tamakoshi A., Tarkaja T., Tarkamaru K.,

RA Takeuchi M., Tamakoshi A., Tarkaja T., Weitzenegger T.,

Winters P., Wabbatt R., Wadheler E., Wedler H., Weitzenegger T.,

RA Winters P., Wabbatt R., Zumstein E., Yoshikawa H., Danchin A.,

The Complete genome sequence of the Gram-positive bacterium Bacillus

RIP First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F. First F.
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE UPP0118 (PERM) FAMILY.
                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                10-OCT-2003 (Rel. 40, Last sequence update)
Hypotherical protein yueF.
Bacillue A.V.
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InterPro; IPR002549; UPF0118.
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                               AGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLGA----IGLIFSTSSLVSGIM 280
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                                                                                                                                                                                                                                                     83 -----AFISASVGPIJTÄQVTGLFNNLPDYIKQIQALTKDLSHSQWFTWMMNQDYVS 134
                                                                                                                                                                                                                                                                                         ---VKHKFTPFTINAVVLLTVG-AAVLGMHTETDKPVHETHKQYITGFLITVAAAVMYAF 183
                                                                                                                                                                                                                                                                                                                    ------ILPLVELAYQ----KAKQTMSYTLVLEF--QLILCLLASIVSVIGMFI 225
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COSMINE=93360813; PubMed=8355609;
COSMINA P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
Venema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
Mol. Microbiol. 8:821-831(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamane K., Kumano M., Kurita K.;
"The 25 degrees-36 degrees region of the Bacillus subtilis chromosome:
determination of the sequence of a 146 kb segment and identification
                                                                                                                                    FSTFLETAGFPVIFIPLL---FSYITRRRSNNVGDSTSFFLIKPRLLIAAVIVGILSGFD
                                                                                                                                                                         33 FIVFISTLFFPMLIAGILYFIFNPVVRLLEKKIPRTLSI-----LLIYLLFIGLL----
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
                                                                                               Indels 123; Gaps
                                                           DB 1; Length 369;
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                      5F86C34CF258C4B8 CRC64;
                                                       ; Score 118.5; DB 1;
; Pred. No. 0.21;
58; Mismatches 116;
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YCXC OR BSU03550.
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MEDLINE=98044033; PubMed=9384377;
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347 LNIVRLIKLRQRSRLEEN 364
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01-FEB-1995 (Rel. 31, Last sequ
10-OCT-2003 (Rel. 42, Last anno
    316 336 PK
369 AA; 40896 MW;
                                                             6.78;
                                                                                 21.4%;
                                                                             l Similarity 21.4%
81; Conservative
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RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., RA Denizot R., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Ghiseppi G., Guy B.J., Hagad K., Haiech J., Harwood C.R., Henaut A., RA Hibbert H., Holsappel S., Hosonos S., Hullo M.F., Itaya M., Jones L., RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., RA Medina N., Mellons S., Mauel C., Medigue C., RA Mone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., RA Pereecan E., Pujic P., Purnelle B., Rapport G., Rey M., Sadaie Y., RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Schied S., Schooter R., Sin B.S., Soldo B., Rapototi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Rateuchi M., Tamakoshi A., Taraka T., Terpstra P., Tognoni A., Tacconi E., Takaji T., Tarpaka T., Terpstra P., Tognoni A., Vari A., Wambutt R., Wadler E., Wedler H., Weitzenegger T., RA, Winners P., Wipat A., Yamamoch H., Yamane K., Yasumoch K., Yasumoch K., Yasumoch K., Yasumoch K., Yasumoch K., Yasumoch K., Yasumoch M., Danchin A., Tamakoshi H., Yamane K., Yoshikawa H., Danchin A., Tamhilia M., Tamachoshi H., Yamane K., Yoshikawa H., Danchin Bacillus F., While M., Tamakoshi H., Yamane K., Yasumoch K., Yasumoch K., The complete genome sequence of the Gram-positive bacterium Bacillus F., Whilia M., Tamakoshi M., Tamamoch M., Yasumoch M., Danchin Bacillus F., Whilia M., Tamakoshi M., Yamanece Of the Gram-positive bacterium Bacillus F., Firm B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AYLPVSTAALIIASQLAFIAIFSFFMVKHKFTPFTINAVVLLTVGAAVLGMHTETDKPVH 161
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the eamA transporter family.
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EMBL; D50453; BAA08989.1; -.
EMBL; Z99105; CAB12149.1; -.
PIR; 140491; 140491.
Subtinist; BG10174; YCXC.
InterPro; IPRO00620; DUF6.
Pfam; PF00892; DUF6; 2.
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277
312 AA;
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Pago protein.
PAGO OR STM1862
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                                       -----YNTAARKMTQRFKLTELTY----IMSAI---GF-----VVFNAIALVRHGAA 208
---GFTVLSVAGVMFIFVMKGVDVESASLKGS------LLILLSALSSAM 168
                      222 GMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLGAIGLIFSTSSLV----S 277
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Feterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
Feterson S.N., Smith H.O., Furchison C.A. III, Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 175:7918-7930 (1993).

-1- FUNCTION: COULD BE PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: Belongs to the binding-protein-dependent transport system permease family. CysTW subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                   Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94075230; PubMed=8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                           Phosphate transport system permease protein pstA homolog
                                                                                                                                                                                                                                                                                                                                                                                                                   "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                654 AA.
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                                                                        GIMISVLLPITE --- VLAVIF 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 136-211 FROM N.A. STRAIN-ATCC 33530 / G-37;
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                                                                                                                                                             STANDARD;
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TRANSMEM 22 4
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TIGR; MG411; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 TPFT-INAVVLLT--VGAAVLGMHTETDKPVHETHKQYITGFLITVAAAV------MYA
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MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                           93; Indels 148; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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STRAIN=ATCC 140285;
MEDLINE=98380520; PubMed=9712687;
Gunn J.S., Belden W.J., Miller S.I.;
"Identification of PhoP-PhoQ activated genes within a duplicated region of the Salmonella typhimurium chromosome.";
Microb. Pathog. 25:77-90(1998).
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: Belongs to the eamA transporter family.
                                                                                                                                                                                                                                                                                        DB 1; Length 654;
                                                                                                                                                                               997BD093F7A907B4 CRC64;
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                                                                                                                                                                                                                                                                            6.5%; Score 115; DB 1
20.6%; Pred. No. 0.61;
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78; Conservative 59; Mismatches
                                                          POTENTIAL. POTENTIAL.
           POTENTIAL
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506 PO
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73525 MW;
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           486
535
613
654 AA;
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MEDLINE=98044033; PubMed=9384377;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 LMIYGETYVNSGLAAIIFANMPVAVLIASVLFINEK---AKLMQIAGLTIAITALTGILL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 LYAYGIAYLPVSTAALIIASQLAFIAIFSFFMVKHKFTPFTINAVVLLIVG-AAVLGMHT 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Indels 32; Gaps
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NCBI_TaxID=1423;
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Wypotherical symporter yjmB.
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235 LQQKANAFQASLVFLIFPLIAV 256
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Microbiology 144:877-884(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome
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                                                                                                                                                                                                                                                                                     EMBL; AE008783; AAL20777.1; -.
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InterPro; IPR000620; DUFG.
Pfam; PF00892; DUF6; 2.
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034961;
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MEDLINE=98044033; PubMed=5384377;
A KURIS F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
A Zevedo V., Bersero M.G. Bessieres P., Bolotin A., Borchert S.,
A Zevedo V., Bersero M.G. Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Borriss R., Boursier L., Caldwell B., Capuano V., Carter N.M.,
Bronillet S., Bruschi C.V., Caldwell B., Capuano V., Daniel R.A.,
Bronisot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Guiseppi G., Guy B.J., Haga K., Haicoh J., Harwood C.R., Henaut A.,
A Guiseppi G., Guy B.J., Haga K., Haicoh J., Harwood C.R., Henaut A.,
A Guiseppi G., Guy B.J., Haga K., Haicoh J., Harwood C.R., Henaut A.,
A Chim S.Y., Coetter P., Koningstein G., Krogh S., Kumano M.,
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A Rager M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
Bato T., Scanlan B., Schleich S., Schroeter R., Scallan B., Schroeter R., Scanlan B., Schroeter R., Yasanrott A.,
A Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
A Tosato V., Uchiyama S., Vandenbol M., Yamane K., Yasanrotti A.,
A Tosato V., Uchiyama S., Vandenbol M., Yamane K., Yasanrotti A.,
A Winters P., Wipat A., Yamamoto H., Yamane K., Yasanrotti A.,
A Winters P., Wipat A., Yamamoto H., Yamane K., Yasanrotti A.,
A Winters P., Wipat A., Yamamoto H., Yamane K., Yashikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Yoshikawa H.F., Zumstein B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B., Waller B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natura 390:249-256(1997).
Natura SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 114; DB 1; Length 459;
23.7%; Pred. No. 0.52;
ive 60; Mismatches 119; Indels 108;
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PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
Hypothetical protein; Transport; Transmembrane; Symport;
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EMBL; Z9910; CAB13088.1; -.
PIR; D69852; D59852.
Subtiliat; BG13205; yjmB.
InterPro; IRR007114; MFS.
InterPro; IRR0071927; NA/Gal_symport.
TIGRFAMB; TIGR007922; Gph; 1.
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Borriss R., Boursler L., Brans A., Braun M., Brighell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
A Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Daniel R.A.,
Brouillet S., Errington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Danizor F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
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A Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
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A Hilbert H., Holsappel S., Hosonos S., Lauber J., Lazarevic V.,
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A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Medina N., Mellado R.P., Mizuno M., Mosell D., Nedigue C.,
A Resecan B., Purnelle B., Roper B., Park S.H.,
A Presecan B., Purnelle B., Roport G., Rey M., Reynolds S.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schiguchi J., Sekowska A., Seror S.J., Sarror P., Shin B.S., Soldo B.,
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Tosconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Yanamoco H., Yanane K., Yasumoto K., Yata K.,
Winters P., Wipat A., Yanamoco H., Yamane K., Yasumoto K., Yata K.,
Winters P., Wipat A., Yamamoco H., Yamane K., Yasumoto K., Yata K.,
Wohlda K., Yoshikawa H.F., Zumstein B., Yoshikawa H., Danchin A.;
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                                                                LASIVSVIGMFIAGDFKQALPKEAREFKLGEALFYVVAVFSAIIWQGFFLGAIGL----
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FNNG-----GKRIWFSTFLETAGPPV----IFI---
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15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical transport protein yetK.
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MEDLINE=98044033; PubMed=9384377;
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 "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Gaps
                                                                                                                                                                                                                                                                                        Transmembrane; Complete proteome.
                       Nature 390:249-256(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the eamA transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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7C6C65F1EDB276B5 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
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59; Mismatches 127;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-FID-164.
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19.8%; Pred. No. 0.4
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                                                                                                                                                                                                                                        Subtilist; BG12867; yetk.
InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Conservative
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                                                            Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Myajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Takeuchi C., Wada T., Matanabe A., Yamada M., Yasuda M., Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
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Pfam; PF00892; DUF6; 2.
Hypothetical protein; Transport; Transmembrane; Complete proteome.
TRANSMEM 15 35 POTENTIAL.
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MEDLINE=97061201; PubMed=8905231;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBUNIT: MAY POLYMERIZE.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- INDUCTION: BY ALLOPHANATE OR ITS NON-METABOLIZED ANALOG OXALURATE.
-i- INDUCTION: BY ALLOPHANATE OR ITS NON-METABOLIZED ANALOG OXALURATE.
-i- SINITARITY: BELONGS TO THE SODIUM:SOLUTE SYMPORTER FAMILY (SSF).
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=S2860 / AB972;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed=8091229;
MEDLINE=94378003; PubMed B., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kuchaba T., Hillier L., W., Jier M., Johnston L., Langston Y., Latreille P., Louis B.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Materston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                             Elberry H.M., Majumdar M.L., Cunningham T.S., Sumrada R.A.,
                                                                                                                                                                                                                                     Cooper T.G.; "Regulation of the urea active transporter gene (DUR3) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 265:2077-2082(1994).
-!- FUNCTION: REQUIRED FOR ACTIVE TRANSPORT OF UREA.
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GermOnline; 139283; -.

$GD; $0001008; DUR3.

GO; GO:0005886; C:plasma membrane; IMP.

GO; GO:0015204; F:urea transporter activity; IMP.

GO; GO:0015840; F:urea transport; IMP.
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TICREAMS; TICREOB13; 888; 1.
PROSITE; PS00456; NA SOLUT SYMP_1; FALSE NEG.
PROSITE; PS00447; NA SOLUT SYMP_2; FALSE_NEG.
PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
(Rel. 28, Created)
(Rel. 31, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                  Saccharomyces cerevisiae (Baker's yeast).
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Pfam: PF00474; SSF; 1.
                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.";
J. Bacteriol. 175:4688-4698(1993).
                                                                                                                                                                                                  MEDLINE=93328673; PubMed=8335627;
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                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                    DUR3 OR YHL016C.
                                                                                                                                      NCBI_TaxID=4932;
     01-FEB-1994
01-FEB-1995
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InterPro; IPR004709; NaH exchang.
Pfam; PF00999; Na H Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.
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                                                                                                                                                                                                                               | :| :| :| :| :| | : : | | : : | | :| | :| | :| | | :| | | :| | :| | | :| | | :| | | :| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| |
                                                                                                                                                                                                       7 IINCIILAIGNCGGPLIMRLYFNNGGKRIWFST-FLETAGFPVIFIPLLFSYITRRSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 VIGMFIAGDFKQALPKEAREFKLGEALFY---VVAVFSAIIWQGFFLGAIGLIFSTSSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBDUTT: Interacts with tescalcin, CHP and CHP2 (By similarity). USUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Not tissue specific.
PTM: Phosphorylated (Possible).
SIMILARITY: Belongs to the Na(+)/H(+) exchanger family.
CAUTION: The number, localization and denomination of hydrophobic domains in the Na(+)/H(+) exchangers vary among authors.
CAUTION: Hydrophobic domains A, B and L are not believed to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 267:9331-9339(1992).

FUNCTION: Involved in pH regulation to eliminate acids generated by active metabolism or to counter adverse environmental conditions. Major proton extruding system driven by the inward sodium ion chemical gradient. Plays an important role in signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Spring.
STRAIN-Spring.
STRAIN-Spring.
MEDLINE=92250539; PubMed=1577762;
Orlowski J., Kandasamy R.A., Shull G.E.;
Orlowski J., Kandasamy R.A., Shull G.E.;
Wholecular cloning of putative members of the Na/H exchanger gene
family. CDNA cloning, deduced amino acid sequence, and mRNA tissue
expression of the rat Na/H exchanger NHE-1 and two structurally
related proteins."
J. Biol. Chem. 267:9331-9339(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VSGIMI-SVLLPITEVL------AVIPYHEKFQAEKGLSLALSLW 313
                                                                                                                                                                   91,
                                                                                                                           DB 1; Length 735;
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10-OCT-2003 (Rel. 42, Last annotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1)
                     POTENTIAL.
POTENTIAL.
GLVAAA -> RLSGCS (IN REF. 1)
PD1252DB838BF5CF CRC64;
                                                                                                                                          ; Pred. No. 1.2;
64; Mismatches 131;
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                                                                                                                       6.3%; Score 111.5;
18.8%; Pred. No. 1.2
                                                             63 G
80616 MW;
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(Rel. 34, Last seq
                                                                                                                                                               Conservative
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639
671
497
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651
58
735 AA;
                                                                                                                                          Local Similarity
Les 66; Conserv
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01-OCT-1996
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch) 134 213 135 FTINAVVLLTVGAAVLGMHTETDKPVHETHKQYITGFLITVAA-AVMYAFILPLVELAYQ 193 53 PRERSIGDUT-----TAPSEPLHHPDDRNLTNLYIEHGAKPVRKAF--PVLDIDYL 101 214 AVCLVGGEQINNIGLLDTLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAV 273 22 ----TEVL 75 IKPRILIAAVIVGILSGFDNYLYAYGIAYLPVSTAALIIASQLAFIAIFSFFMVKHKFTP 16 IFPSLLVVVALVGLLP----VLRSHGLQLNP--TASTIRGSE-----P -----DFKQALPKEAREFKLGEALFYVVAVFSAIIWQGPFLGAIGLIF 159 FLQSDVFFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVV---GTLWNAFFLG--GLLY TIGRFAMB; TIGR00840; b_cpal; 1. Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport; (POTENTIAL) Indels 127; 6.3%; Score 111.5; DB 1; Length 820; 19.7%; Pred. No. 1.3; tive 49; Mismatches 89; Indels 127 194 KAKQTMSYTLVLEFQLILCL------LASIVS-----VIGMFIAG-EXTRACELLULAR (POTENTIAL) F (MSA) (POTENTIAL). EXTRACELLULAR (POTENTIAL) H (M6) (POTENTIAL). L, HYDROPHOBIC. EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL)
D (M4) (POTENTIAL). EXTRACELLULAR (POTENTIAL) J (M8) (POTENTIAL). K (M9) (POTENTIAL). EXTRACELLULAR (POTENTIAL) -binked (GLCNAC. . .) (P CYTOPLASMIC (POTENTIAL). G (M5B) (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL). CYTOPLASMIC (POTENTIAL).
A (MI) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
B (MZ) HYDROPHOBIC. D (M4) (POTENTIAL).
CYTOPLASMIC (POTENTIAL) B (M2) HYDROPHOBIC. CYTOPLASMIC (POTENTIAL) M (M10) (POTENTIAL). CYTOPLASMIC (POTENTIAL) ---SSLVSGIMISVLLPI----(POTENTIAL). C (M3) (POTENTIAL). (POTENTIAL) 292 AVIFYH--EKFQAEKGLSLALSLWGFVSYF 319

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P93010 arabidopsis
Q94gb1 arabidopsis
Q9fz95 arabidopsis
Q9k72 oryza sativ
Q9k72 arabidopsis
Q9726 arabidopsis
Q7x7p4 oryza sativ
Q9724 arabidopsis
Q9724 arabidopsis
Q92uh3 arabidopsis
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Q8774 arabidopsis
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1 MKNGLIIINCIILTIGTCGG.......DKPQPPETELPILPVSDYVA 356
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         GenCore version 5.1.6
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                              SEQUENCE FROM N.A.

Yamada K., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,

Yamada K., Chan M.M., Chang C.H., Toriumi M., Wong C., Wu H.C.,

Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Yu G., Yama S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,

Southwick A., Tripp M.G., Wu T., Satou M., Seki M., Shinn P.,

Theologis A.,

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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO21044, AAPS4317.1;

EMBL, AKIJ7664; BAC42317.1;

EMBL, EMBL, BALO5504; AAO63924.1;

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RRGNRNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIG
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
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PEam; PF00892; DUF6; 1.
SEQUENCE 356 AA; 39280 MW; FA2701E954CF797B CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO; GO:0016020; C:membrane; IEA.
InterPro; IPR004853; DUF250.
InterPro; IPR000620; DUF2
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                          Gaps
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1.6e-132;
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62.9%; Pred. No. 5.3e-83;
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Score 1792;
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PIR, B84749; B84749.
Interpro, IPR004853; DUF250.
BERN, PF03151; DUF250; 1.
SEQUENCE 356 AA; 39201 MW;
    99.78;
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    Query Match
Best Local Similarity 99.7
Matches 355; Conservative
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STRAIN=cv. Columbia;
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181 VVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFK---- 236
                                                                                                                                                                                                                                                                                                       LLPVTEVFAVVCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPIL 349
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A Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
B Halei H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,
B Buehler E., Chao C., Chin C., Chiou J., Choi E., Gonzalez B.,
Howng B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M.,
Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,
Loriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
Lubmitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
BRBL; AC021044; AAF98433.1; -.
BRBL; C86408; C86408.
R InterPro; IPR004853; DUF250.
R InterPro; IPR004853; DUF250.
R Pfam; PF03151; DUF250; 1.
                                                                            301 CFREKFQAEKGVSLLLSLWGFVSYFYGEFKSG--KKVVDKPQPPETELPIL--PVSD 353
                                                                                                                                                                      -----VIAREAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISV
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NCBI_TaxID=3702;
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63.1%; Score 1134.5; DB 10; Lengt
Best Local Similarity 59.9%; Pred. No. 5.2e-81;
Matches 214; Conservative 66; Mismatches 66; Indels
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PVTDYVA 358
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                                                                                                                                                                                                                                                             TOLAFNALFAFLLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMT 180
                                                                                                                                                                                                                                                                                                115 AQLGFTALFAFFWVKQKFTPFTINAIVLLTGGAVVLALNSDSDKLANETHKEYVVGFIMT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                -----VIAREAREFKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISV 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLPVTEVFAVVCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPIL 349
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                                  VVAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFK----
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
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358 AA; 39461 MW; 69709A0EAGECDGA8 CRC64;
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11 Similarity 62.9%; Pred. No. 5.4e-83;
231; Conservative 45; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358
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EMBL, AFOT8532; AAKG1813.1; InterPro; IPR004853; DUF250.
InterPro; IPR004853; DUF250.
NON TER 358 A8; 39461 MW; 69709A0E
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FYHEKFQAEKGLSLALSLWGFVSYFYGEIKSGEDKRRIQQEESQETEQSSLSRPISE 350

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124 AFNALFAFILIVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVA 183
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                             ; Score 676.5; DB 10; Length 399;
; Pred. No. 4.5e-45;
63; Mismatches 119; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFAVVCFREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKVVDKPQPPETELPI 348
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                     SEQUENCE FROM N.A. Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski Currie J., Collura K.;
                                                                                                                                                                                                                                           "Rice Genomic Sequence.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC121489; AAN64138.1; -.
InterPro; IPR004883; DUF250.
Pfam; PF03151; DUF250; 1.
Hypothetical protein.
SEQUENCE 399 AA; 41487 MW; D180480A4081416A CRC64;
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Last annotation update)
                                                                 Last sequence update)
Last annotation update)
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                       399 AA
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01-MAY-2000 (TrEMBLrel. 13, Last seq
                                                     Created)
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                                                   (TrEMBLrel. 23, C
(TrEMBLrel. 23, I
(TrEMBLrel. 24, L
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                         PRELIMINARY;
                                                                                              Hypothetical protein.
0J1217B09.4.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                   NCBI_TaxID=39947;
                                                      01-MAR-2003
                                                                  01-MAR-2003
01-JUN-2003
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RESULT 6
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SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Yamada K., Chan M.M., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.,
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC004135; AAD32940.1; -.
EMBL; BT004160; AAO42180.1; -.
EMBL; BT004160; AAO42180.1; -.
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Yamada K., Chanm M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Yamada K., Chanm M.M., Tang C., Toriumi M., Wong C., Wu H.C.,
Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Saltou M., Seki M., Shinn P.,
Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Comu L., Comway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Lee J., Lenz C., Li J., Sakano H., Schwartz J., Southwick A., Thaveri M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                              Genomic sequence for Arabidopsis thaliana BAC T17H7 from Chromosome
                                                                                                                                                                                                                                                                                                                                                                                       Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Kim C., Walker M., Altafi H., Araujo R., Conn L., Conway A., Gonzalez A., Hansen N., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu, G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
           Dewar K., Feng J., Kim C., Li Y., Sun H.,
Kurtz D., Oji O., Shen Y.K., Toriumi M.,
Davis R.W., Federspiel N.A., Theologis A.,
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell
Feldmann K.;
Fildmann K.;
Fill-Length, CDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theologis A.;
"Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                               Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
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SEQUENCE FROM N.A.
Buehler E., Shinn P., D
Conway A., Conway A., K
Vysotskaia V., Yu G., D
                                                                                                                                                                                                                           Ecker J.R.;
Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Bollm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk K., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narueaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                  14;
                                                                                                                        Length 382;
                                                                                                                    ; Score 553; DB 10; Length 3; Pred. No. 2.1e-35; 65; Mismatches 132; Indels
                                                                                        42320 MW; E030A23A8C834ACA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2003 (TrEMBLrel. 24, Last annotation update)
T12C22.2 protein (Hypothetical protein)
T12C22.2 OR AT1G44750, T12C22.2 OR AT1G44750.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                     36.3%;
GO; GO:0016020; C:membrane;
InterPro; IPR004683; DUP250.
InterPro; IPR006620; DUF6.
Pfam; PF03151; DUP250; 1.
Pfam; PF00892; DUF6; 1.
                                                                                                                                                  Matches 120; Conservative
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                                                                        Hypothetical protein. SEQUENCE 382 AA; 4
                                                                                                                                   Local Similarity
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                                                                                                                     Query Match
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SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 FKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
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Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,
Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,
Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
14-pochetical protein.
17-pa21.70 OR AT4G18220.
Arabidopsis thaliana (Mouse-ear cress).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 379 AA; 41289 MW; FIED85A70FAD7001 CRC64;
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Best Local Similarity 34.4%; Pred. No. 3.5e-35;
Matches 119; Conservative 74; Mismatches 133;
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Pfam; PF03151; DUF250; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 SYVMNIVWTAVTWQVFSIGCTGLIFELSSLFSNAISALGLPVVPILAVIIFHDKONGLKV 295
                                                                                                                                                                                                                                                                                                                                                                                                                     67 LRNRALVY------IVLGELVGAACYLYSIGELYLPVSTLSLICASQLAFTAFFSY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINSOKLTPIIINSLFILTISSTLLAFNNEESDSKKVTKGEYVKGFVCTVGASAGFGLLL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 NKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLVKOKFTPFSINAVVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFIL 191
                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                     12 ILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAE
                                                                                                                                                                                                                                                                                                                   Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
T9A21.60 OR AT4G18210.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                           30.3%; Score 545.5; DB 10; Length 344; 35.1%; Pred. No. 7.2e-35; artive 69; Mismatches 142; Indels 11;
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Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley
Bancroft I., Mewes H.W., Mayer K., Schueller C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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SUD Arabidopsis sequencing project;
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SUD Aracted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21713; CAA16793.1; -.
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EMBL; AL021713; CAA16794.1; -.
EMBL; AL161548; CAB78824.1; -.
PIR; T04924; T04924.
InterPro; IPR004853; DUF250.
PYam, PF03151; DUF250; 1.
Hypothetical protein.
SEQUENCE 344 AA; 37819 MW; 28795F066738D9B1 CRC64;
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348 AA; 38556 MW;
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InterPro; IRR004853; DUF250.
Pfam; PF03151; DUF250; 1.
Hypothetical protein.
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Best Local
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Length 348;

DB 10;

Score 543;

30.2%;

Query Match

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                                                                                                         17 TCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKT 76
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Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
In Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y., Li G., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
Submitted (SPP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALG62557; CAE03376.1;
EMBL, ALG62557; CAE04314.1;
SEQUENCE 751 AA; 79987 WW; 714C08319D7B5FDI CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 IVITGIIMQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLL
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01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
05-0cr-2003 (TrEMBLrel. 25, Last annotation update)
05-0cr-2003 (TrEMBLrel. 05, Last annotation update)
05-0cr-2003 (TrEMBLrel. 05, Last annotation update)
05-0cr-2003 (TrEMBLrel. 05, Last annotation)
05-0cr-2003 (Trecheophyta, Smbryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
05-0cr-2003 (Tracheophyta, Liliopsida, Poales, Poaceae)
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Best Local Similarity 34.4%; Pred. No. 1.1e-34;
Matches 116; Conservative 69; Mismatches 130; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 AIWGFTSYVYOQYLDDKNLKKNHEITTTESPDPPEAE 341
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Best Local Similarity 33.9°
Matches 112; Conservative
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308 VYIIGVVGLIFESSSVFSNSITAVGLPIVPVVAVIVFHDKMNASKIFSIILAIMGFISFV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 VVLLTVGIGILALHSDGDKPAKESKKEYVVGFLMTVVAALLYAFILPLVELTYKKARQBI 205
                                                                                                                               266 GFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFREKFQAEKGVSLLLSLWGFVSYF 325
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                     206 TFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREAREFKIGGSVFYYALIVITGIIWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S LIIINCIILTIGTCGGPLLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 RNPNNAENKRKTKLFLMET-PLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AFNALFAFLLVKQKFTPFSINAVVLLTVGIGILALHS--DGDKPAKESKKEYVVGFLMTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 VAALLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 GAAGLFAAYLPVMELVYRKAVSG-GFRMAVEVQVIMQAAATALAVAGLAAAGGWK---EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0019E03.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; APR003335; BAB90042.1;
EMBL; AP004363; BAC01243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone:B1144G04.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03151; DUF250; 1.
SEOUENCE 372 AA; 38794 MW; 6759730D536EC4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                         368 YQHYLDEKKLKTSHTSPVGDPHLLPAEE 395
                                                                                                                                                                                                326 YGEFKSGKKVVDKPQPPETELPILPVSD 353
                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Best Local Similarity 36.8
Matches 123; Conservative
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Q8S170;
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                                                                                                                                                                                                                  244
                                                                                                                                                                                                                                                                                                     86 FIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLLVKQKFTPFSINA 145
                                                                                                                                                                                                                                                                                  FKIGGSVFYYALIVITGIIWQGFFLGAIGIVFCASSLASGVLISVLLPVTEVFAVVCFRE 304
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               64
                               49 WVAVDVFFLIAGQTSATLIGRYYYTGGGRSKWISAFVRTAGFPILFFTLFFF-----PS
                                                                                                                                                                 216 CTYSLILALMQLTFETIIKKHTFSAVLNMQIYTALVATAASVVGLFASGEWRSLRGEMNA
                                                                                                          KSPSSCTNTPMAK-----LAVIYIVLGLIIAADDMMYTGGLKYLPASTYSLICASQLA
                                                                                                                                                                                                               LLYAFILPLVELTYKKARQEITFPLVLEIQMVMCLAATFFCVIGMFIVGDFKVIAREARE
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                                                                            RNPNNAENKRKTKLFLMETPLFIASIVIGLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRGNRNPNNAENKRKTKLFLMETPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1128;
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%; Pred. No. 2e-33;
ive 72; Mismatches 133; Indels
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUDMILLED (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21713; CAA16792.1; -.
EMBL; AL161548; CAB78822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1128 AA; 124621 MW; 9B1B88BFA0DE9E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1128 AA
                                                                                                                                                                                                                                                                                                                                                     305 KFQAEKGVSLLLSLWGFVSYFYGEFKSGKK 334
                                                                                                                                                                                                                                                                                                                                                                       335 RANGVKIVAMLIAIWGFISYLFQHYLDGKK 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequenc
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Hypothetical protein.
19A21.50 OR AT4G18200.
Arabidopsis thaliana (Mouse-ear cress).
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Pfam; PF03151; DUF250; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 1128 AA;
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295 SSYIYGSSSS 304
                                                                 Q8RY74;
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                                  RESULT 15
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
MEDLIRE=20081487; PubMed=10617197;
MEDLIRE=20081487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea M.E., Feldblyum T.V.,
Buell C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLTRLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRGNRNPNNAENKRKTKLFLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.6%; Score 531.5; DB 10; Length 36.8%; Pred. No. 8.2e-34; ive 67; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005967; AAD03383.1; -.
PIR; A84634; A84634.
InterPro; IPR004853; DUF250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03151; DUF250; 1.
SEQUENCE 315 AA; 33847 MW; C7658FFABD4B3814 CRC64;
                                                                                                                                     01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                    FREKFQAEKGVSLLLSLWGFVSYFYGEFKSGKKV 335
                                               Best Local Similarity 36.8
Matches 114; Conservative
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                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
                                                                                                                                                                       At2g24220 protein.
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                                                                                            RESULT 14
Q9ZUH3
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78 LFLMETPLF--IASIVI--GLLTGLDNYLYSYGLAYLPVSTSSLIIGTQLAFNALFAFLL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 PLATVIGRLYYENGGKSTYVVTLLQLIGFPVL---ILFRFFSRIR------QPKSTD 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 PLIT----RLYFTNGGKRIWFMSFLSTAGFPIILIPLLVSFLSRRRGNRNPNNAENKRKTK 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., "Arabidopsis Full Length cDNA Clones.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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"Arabidopsis Open Reading Frame (ORF) Clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
29.3%; Score 526.5; DB 10; Length 377;
Best Local Similarity 35.2%; Pred. No. 2.4e-33;
Matches 118; Conservative 70; Mismatches 124; Indels 23;
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SROUENCE 377 AA; 41786 MW; B77A09A4289859AB CRC64;
                                                                                          Last sequence update)
Last annotation update)
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Z
                                                              Created)
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                                                InterPro; IPR004853; DUF250.
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341 IILAIWGFLSFVYQHYLDEKKLKTCQTKPVEEETQ 375

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